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Sequence 111, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 17, App Sequence 17,
                                                                                                                                                                    August 27, 2005, 08:48:34; Search time 106.452 Seconds (without alignments) 4565.212 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                           1 gcaatcgatggggcatcctt.......ccatcaagaagattatggtt 297
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-808-148-2

US-09-020-956-111

US-09-439-313-111

US-09-325-616A-111

US-09-159-812-111

US-09-159-812-111

US-09-159-812-111

US-09-115-455-111

US-09-115-455-111

US-09-115-45-111

US-09-651-13-111

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US-09-61-13-111

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US-09-148-545-14
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US-09-115-453-17
US-09-688-489-17
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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5	272.8	91.9	740	4	US-09-759-143-17	Sequence 1	
30	272.8	91.9	740	4	US-09-651-236-17		
31	263.8	88.8	729	m	US-09-020-956-13	Sequence 1	
32	263.8	88.8	729	m	US-09-030-607-13	Sequence 1	
33	263.8	88.8	729	ო	US-09-439-313-13	_	
34	263.8	88.8	729	ო	US-09-352-616A-13	Sequence 1	
35	263.8	88.8	729	М	US-09-232-149A-13	_	
36	263.8	88.8	729	4	US-09-159-812-13	_	
37	263.8	88.8	729	4	US-09-636-215-13	Sequence 1	
38	263.8	88.8	729	4	US-09-685-166A-13	Sequence 1	
39	263.8	88.8	729	4	US-09-115-453-13	_	
40	263.8	88.8	729	4	US-09-688-489-13	-	
41	263.8	88.8	729	4	US-09-679-426-13	Sequence 1	
42	263.8	88.8	729	4	US-09-759-143-13	Sequence 1	3, Ap
43	263.8	88.8	729	4	US-09-651-236-13	Sequence 1	
44	220.6	74.3	801	'n	US-09-020-956-16	Sequence 1	
45	220.6	74.3	801	٣	US-09-030-607-16	Sequence 1	6, App.

### ALIGNMENTS

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Sequence 1, Application US/09308984

Patent No. 6388065

GENERAL INFORMATION:
APPLICANT: Nest, Matthias
APPLICATION: DIA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
FILE REFERENCE: SCHU 204 (09902857)
CURRENT FILING DATE: 1999-09-03
PRIOR PAPLICATION NUMBER: US/09/3308,984
PRIOR PILING DATE: 1996-11-12
PRIOR PLING DATE: 1996-11-12
PRIOR FILING DATE: 1997-11-27
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 1
LENGTH: 297
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100.0%; Pred. No. 2.4e-79;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 297; Conservative
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CORGANISM: Homo sapiens
US-09-308-984-1
US-09-308-984-1
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RESULT 2 US-08-808-148-2 ; Sequence 2, Application US/08808148

BEST AVAILABLE COPY

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Patent No. 6261562
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
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                    GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer
APPLICANT: Goli, Surya
APPLICANT: Goli, Surya
APPLICANT: And, Hong Wolfe
TITLE OF INVENTION: NOVEL HUMAN TUMOR-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                          ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF-0218 US
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US-09-020-956-111
; Sequence 111, Application US/09020956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Billings, Lucy J. 749
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0;
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-85-055
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 933 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Matches 284; Conservative
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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSNOT26
CLONE: 2187263
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## 2/9/48 File

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; Sequence 111, Application US/09030607; Patent No. 6262245; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 rescricascarricardacerrecresias rescricas de sos
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                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-PEB-1998
CLASSIP FORD.
ATTORNEY/ACTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 62-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1289 base pairs
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Best Local Similarity 99.3
Matches 284; Conservative
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STRANDEDNESS: sing
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ORIGINAL SOURCE:
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APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Wi Jiang, Yuqui
APPLICANT: Wi Jiang, Yuqui
TILLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FASESEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 1289;
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99.3%; Pred. No. 8e-75;
ive 0; Mismatches 2; Indels 0;
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: Day, CIRCH
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPRENENCE: 210121-427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 111
LENGTH: 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 TGGCTGAGCACTTCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAA 505
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Best Local Similarity 99.3
Matches 284; Conservative
                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapien
US-09-439-313-111
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; ORGANISM: Homo sapien
US-09-352-616A-111
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Matches 284; Conserv
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                                                                                                                                                                                                                                                                                                          TYPE: DNA
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Pred. No. 8e-75; |
0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPRANTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 111, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Reed, Steeven G.
APPLICANT: Reed, Steeven G.
APPLICANT: Ralos, Michael
APPLICANT: Fanger, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.3%;
Matches 284; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1289 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                Seattle
                                                                                                                                                                       ZIP: 98104
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US-09-439-313-111
                                                                                                                        STATE: W.
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CURRENT FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 306
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 111.
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Sequence 111, Application US/09636215
Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Witcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Harlocker, Susan L.
APPLICANT: Ratlos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Scaig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Oby, Craig H.
APPLICANT: Objector, Darrick
                                                                                                                                                                                                                             Best Local Similarity 99.3 Matches 284; Conservative
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; ORGANISM: Homo sapien
US-09-636-215-111
                                                                                                                  TYPE: DNA
ORGANISM: Homo sapien
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                                                                                            LENGTH: 1289
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APPLICANT:
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TIGICARGETGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGTCTTTGCTCTTTGCTTTTCC 339
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                                                                     TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
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                                                                                                                                                                                                                                                                                                                                                              RESULT 7
US-09-232-149A-111
Sequence 111, Application US/09232149A
Sequence 111, Application US/09232149A
Sequence 111, Application US/09232149A
Setent No. 6455611
GENERAL INFORMATION:
APPLICANT: Nu. Janagchun
APPLICANT: Mitcham, Jennifer Lynn
TILLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT PILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FaetSEQ for Windows Version 3.0
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Sequence 111, Application US/09159812A

Sequence 111, Application US/09159812A

GENERAL INC. 613872

APPLICANT: Xu, Jiangchun

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF

TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.428C5

CURRENT APPLICATION NUMBER: US/09/159,812A
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Best Local Similarity 99.3
Matches 284; Conservative
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US-09-232-149A-111
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LENGTH: 1289
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95.2%; Score 282.8; DB 4; Length 1289; 99.3%; Pred. No. 8e-75; 2; Indels 0;
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT PEPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 111
LENGTH: 1289
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400 TCCTCCTCATCTTCATTGCTGAGGTTGCTGCTGCTGTGGTGTTGGTGTACACCACAA 459
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Patent No. 6657056

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: AL, Jiangchun
APPLICANT: AL, Jiangchun
APPLICANT: AL, Jiangchun
APPLICANT: AL, Jiangchun
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
TITLE OF INVENTION: METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C4
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228

SOFTWARE: FEASTSEQ for Windows Version 3.0

SEQ ID NO 111
LENGTH: 1289
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Pred. No. 8e-75;
0; Mismatches 2; Indels 0;
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PAPLICANT: Micham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

TITLE OF INVENTION: COMPOUNDS FOR THEIR USE

TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

TITLE OF INVENTION: 21012.142702

CURRENT APPLICATION NUMBER: US/09/688,489

CURRENT FILING DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 338

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 111

LENGTH: 1289
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Best Local Similarity 99.3
Matches 284; Conservative
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ORGANISM: Homo sapien
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CORGANISM: Homo sapien
US-09-688-489-111
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CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGGCCACTGTCGTCCAGTGCCATGCAGT
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hebler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSIATE CANCER
FILE REFERENCE: 210121,427C21
CURRENT APPLICATION UNDERS: US(09/685,166A
CURRENT FILING DATE: 2000-10-10
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Pred. No. 8e-75;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 IGGCIGAGCACTICCCGACGTIGCTGGTGCCTGCCATCAAGAA 287
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SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Best Local Similarity 99.3<sup>3</sup>
Matches 284; Conservative
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ORGANISM: Homb sapien
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340 TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCTTCATCC 399
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                                                                                       TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCATAA
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APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Weng, Aijun
APPLICANT: Weng, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILIAG DATE: 2001-01-12
NUMBER OF SEC ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 111
LENGTH: 1289
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Pred. No. 8e-75;
0; Mismatches 2; Indels 0;
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; Sequence 111, Application US/09759143
; Patent No. 6800746
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Best Local Similarity 99.3%;
Matches 284; Conservative
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COGANISM: Homo sapien
US-09-759-143-111
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APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Odd.ck, Thomas S.
APPLICANT: Odd.ck, Millian A.
APPLICANT: Wadg, Aijun
APPLICANT: Wadg, Aijun
APPLICANT: Wadg, Aijun
APPLICANT: Unwenflow: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: LONGORIES OF PROSTATE CANCER
FILE REFERENCE 210121.42720
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT APPLICATION NUMBER: US/09/679,426
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 0111
FURNIT OF 10 111
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                      Length 1289
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95.2%; Score 282.8; DB 4; Length 1
Best Local Similarity 99.3%; Pred. No. 8e-75;
Matches 284; Conservative 0; Mismatches 2; Indels
                                                                2; Indels
                  Score 282.8; DB 4;
Pred. No. 8e-75;
    95.2%; Scor.
99.3%; Pred. No. ec.
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 111, Application US/09679426
; Patent No. 6759$15
                                       Best Local Similarity 99.3
Matches 284; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; GENERAL INFORMATION:
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62 TIGHCANGGRAGGTACTICCTCATCGCAGCCGGCGTTGTGGTCTTGGTCTTGGTTTCC 121
280 TIGHCAACGTGGGCTACTICCTCATCGCAGCCGGCGTTGTGGTCTTGGTCTTGGTTTTCC 339
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             US-09-651-236-111

Sequence 111
Sequence 111
Sequence 111
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Wang, Ailun
APPLICANT: Wang, Steiky, Yasir A.W.
APPLICANT: Wang, Ailun
APPLICANT: Wang, Ailun
APPLICANT: Steiky, Yasir A.W.
APPLICANT: Wang, Ailun
APPL
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95.2%; Score 282.8; DB 4; Length 1289;
Best Local Similarity 99.3%; Pred. No. 8e-75;
Matches 284; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460 TGGCTGAGCACTTCCTGACGTTGCTGGTGCCTGCCTCCATCAAGAA 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-651-236-111
US-09-651-236-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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August 27, 2005, 07:00:48; Search time 355.016 Seconds (without alignments) 4952.347 Million cell updates/sec Run on:

ÚS-10-079-954-1

1 gcaatcgatggggcatcctt......ccatcaagaagattatggtt 297 Perfect score: Sequence:

4390206 segs, 2959870667 residues Gapop 10.0 , Gapext 1.0 Searched:

IDENTITY NUC

Scoring table:

8780412 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_16Dec04:\* Database :

geneseqn2003ds:\* geneseqn2004as:\* geneseqn2003cs:\* geneseqn2001bs:\* geneseqn2002as:\* geneseqn2002bs:\* geneseqn2001as: geneseqn2003bs:\* geneseqn1980s:\* geneseqn1990s:\* geneseqn2003as:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:

SUMMARIES

# æ

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
1	297	100.0	297	7	AAV15588	Aav15588 Human HPK
7	282.8	95.2	513	ß	AAF93382	Aaf93382 Lung carc
3	282.8	95.2	635	4	AAI29471	
Ω 4	282.8	95.2	.632.	80	ABZ33657	Abz33657 Human col
S	282.8	95.2	792	9	ABK29835	Abk29835 Colon ade
9	282.8	95.2	933	~	AAV54014	Aav54014 Nucleotid
7	282.8	95.2	1076	9	ABS76533	Abs76533 cDNA enco
80	282.8	95.2	1076	10	ADB75600	Adb75600 Prostate
0	282.8	95.2	1076	13	ADR25330	Adr25330 Breast ca
10	282.8	95.2	1076	13	ADR65868	Adr65868 Human pro
11	282.8	95.2	1076	13	ADR66771	Adr66771 Human pro
12	282.8	95.2	1077	13	ADQ85081	Adq85081 Human tum
13	282.8	95.2	1154	ø	ABS76532	u
14	282.8	95.2	1154	10	ADB75598	Adb75598 Prostate
15	282.8	95.2	1278	11	ADN39285	Adn39285 Cancer/an
16	282.8	95.2	1288	~	AAV48113	Aav48113 Nucleotid
c 17	282.8	95.2	1288	2	AAD62626	Aad62626 DNA #4 us
18	282.8	95.2	1288	10	AAD62609	Aad62609 Human rec
19	282.8	95.2	1289	~	AAV58587	Aav58587 Prostate
20	282.8	95.2	1289	7	AAV61202	Aav61202 Full leng

Abs71255 Human pro	Aah93466 Human pro	Aas63558 Human pro	Aah02531 Prostate	Aah84780 Human pro	Aaf86954 Human P50	Aca59367 Prostate	Aas10109 Human pro		Abs58639 Prostate	Acc95094 Prostate	Adb13561 Human pro	Adg25977 Human pro	Human i	Adr44012 Human bre	Aav34225 Human sec	Acd08096 cDNA enco	Aav34157 Human sec	Acd08028 cDNA enco	Adall015 Human cDN	Aaz95011 Cancer sp	Abv23358 Human pro	Adl62990 Human ova	Aav30916 Human sec	Aaf98395 Human cDN
3 ABS71255	4 AAH93466	4 AAS63558	4 AAH02531	4 AAH84780	4 AAF86954	5 ACA59367	5 AAS10109 ·	6 ABL94930	6 ABS58639	8 ACC95094	10 ADB13561	10 ADG25977	3 AAA06350	13 ADR44012	2 AAV34225	8 ACD08096	2 AAV34157	8 ACD08028	9 ADA11015	3 AAZ95011	5 ABV23358	5 ADL62990	2 AAV30916 .	5 AAF98395
1289	1289	1289	1289	1289	1289	1289	1289	1289	1289	1289	1289	1289	1290	1306	1324	1324	1376	1376	1456	1533	1603	1603	1605	1605
95.2	95.2	95.2	95.2	95.2	95.2	.95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2	95.2
282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8	282.8
21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

BP. AAV15588 standard; DNA; 297 AAV15588; RESULT 1 AAV15588 

(first entry) 02-JUL-1998

Human HPK-1A C4.8 DNA.

Cervical cancer; treatment; diagnosis; passage cell; lesion; human foreskin keratinocyte cell line; HPK-1A; antibody; smear; ss.

Homo sapiens.

DE19649207-C1

26-FEB-1998.

96DE-01049207. 27-NOV-1996;

96DE-01049207 27-NOV-1996; (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

Nees M; Duerst M,

WPI; 1998-121623/12. P-PSDB; AAW47275.

Nucleic acid characteristic of late or early passage cells immortalised by papilloma virus - and related polypeptide(s) and antibodies, used for diagnosis and treatment of cervical cancer and assessing potential for progression of cervical lesions.

Claim 2; Fig 1; Bpp; German.

This sequence, C4.8, is derived from a human papillomavirus (HPV) immortalised human foreskin keratinocyte cell line HPK-1A and is characteristic of late or early passage cells. This sequence is used in a method for assessing the potential for progression of cervical lesions. Antibodies generated against the encoded polypeptide are used for diagnosis of cervical cancer and to assess potential for lesion

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progression. Antibodies can also be used therapeutically by inhibiting the polypeptide. Antisense molecules based on the nucleoride sequence are used to inhibit expression of the protein. Detecting polypeptides, or related RNA, characteristic of late passage cells (which are potentially malignant) in cervical smears is a reliable way of assessing progression
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                                                                                                                                                                                                                                                                                                                                                                                      CTCCTCCTCCTCATCTTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCATA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid molecule encoding a SRT polypeptide is useful for production of recombinant SRT polypeptides, gene mapping, diagnosing genetic disorders and for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAAGATTATGGTT 297
                                                                                                                                                                                                     GCAATGGGGGCATCCTTTCTGAAGATCTTCGGGGCCACTGTCCAGTGCCATGCAG
                                                                                                                                                                                                                                             TTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGTCTTTGCTCTTTGGTTTTC
                                                                                                                                                                                                                                                              TTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGGCTTTGCTCTTGCTTTTGTTTC
                                                                                                                                                                                                                                                                                                   CTGGGCTGCTATGGTGCTAAGACTGAGAGGGAAGTGTGCCCTCGTGACGTTCTTCTTCATC
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                                                                                                                                                                                     GCAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCGAGTGCCATGCAG
                                                                                                                                                          Gaps
                                                                                                                                                          ;
                                                                                                                              Length 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; SRT; gene therapy; gene mapping; tissue typing; ss.
                                                                                                                                                         0; Indels
                                                                                                  Seguence 297 BP; 46 A; 79 C; 80 G; 92 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lung carcinoma cDNA encoding SRT protein SEQ ID 203
                                                                                                                           Query Match 100.0%; Score 297; DB 2; Best Local Similarity 100.0%; Pred. No. 4.5e-76; Matches 297; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Fig 203; 663pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA; 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baker KP, Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-112729/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF93382 standard;
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                                                                                                                              Query Match
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Sequences AAF93180 - AAF93743 represent polynucleotide sequences encoding human SRT proteins. The CDNA sequences are isolated from various fiferent human tissue CDNA libraries. The invention relates to a method for detecting cDNA encoding an SRT protein, a vector containing CDNA encoding SRT, a host cell transformed with the vector, an isolated SRT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis; colon cancer; colon tumour; immunogenic;
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polypeptide, and an antibody which binds to SRT. The polynucleotide sequence can be used in gene therapy and is useful in the recombinant production of SRT polypeptides as a hybridisation probe to screen libraries to isolate cDNAs with sequence identity to SRT polypeptides, the map the gene encoding the SRT polypeptides and analysing genetic disorders, tissue typing and disease tissue detection. The SRT polypeptides polynucleotide sequences can be used in polymerase chain reaction, screening for new therapeutic molecules and generation of antisense RNA
                                                                                                                                                                                                                                                                                                                                                      TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC
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                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colon tumour related determined cDNA sequence for clone R0098:F06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stolk JA;
                                                                                                                                                                                             °
                                                                                                                                                                Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 TGGCTGAGCACTTCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAA 384
                                                                                                                                       Sequence 513 BP; 97 A; 135 C; 129 G; 152 T; 0 U; 0 Other;
                                                                                                                                                                Score 282.8; DB 5; Length
Pred. No. 7.2e-72;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               242 TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meagher MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy; vaccine; colonic cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.2%;
                                                                                                                                                                                             284; Conservative
                                                                                                                                                                                Similarity
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Best Local S
                                                                                                                and DNA
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The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) and be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) corpression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying. (II) must be used to treat disorders associated with decreased expression by rectifying or to treat disorders associated with decreased expression by rectifying or TCAPE by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the calls to be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of the castoriative therapy. (I) may also be used as antigens in the production of antibodies against TCAPE and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and antagonists may also be used as diagnostic agents for detecting the antibodies may also be used as diagnostic agents for detecting the considered and amino acid sequences given in the exemplification of the reconstruction of the exemplification of the exemplification of the exemples of the production of the exemple of the production of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCATAA 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGT
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Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer.
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Pred. No. 7.8e-72;
0; Mismatches 2; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human colon tumour cDNA for clone R0098:F06 SEQ ID NO:1025.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 635 BP; 173 A; 162 C; 165 G; 134 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                       Claim 2; Page 414; 472pp; English
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WO200283070-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396
                                                                                                                                                                                                     Xu J, Lodes MJ, Secrist H, Benson DR, Meagher MJ, Stolk JA;
Wang T, Jiang Y, Smith CL, King GE, Wang A, Clapper JD, Skeiky YAW;
Panger GR, Vedvick TS, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                     present invention describes compounds (I) for the immunotherapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        575 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGT
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                                                                                                                                                                                                                                                                                                                     New polynucleotide, useful for the preparation of a composition for stimulating an immune response against, or treating, cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 8; Length 635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; colon adenocarcinoma; colon cancer; tumour; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335 rescreascarrecreacerrecresrandescreecerecearcaasaa 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 635 BP; 173 A; 162 C; 165 G; 134 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.2%; Score 282.8; DB 8; Length (99.3%; Pred. No. 7.8e-72; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA
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                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 415; 537pp; English
                                                                                       10-APR-2001; 2001US-00833263.
03-AUG-2001; 2001US-00922217.
19-DEC-2001; 2001US-00025380.
                                                     09-APR-2002; 2002WO-US011475.
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                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                   WPI; 2003-067548/06.
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Best Local Similarity
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               24-0CT-2002
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The invention relates to an isolated polynucleotide (I) encoding a polypeptide (II) comprising a portion of a colon tumour protein. A new polypeptide (III) that hybridises to (I) is useful for determining the presence of a cancer in a patient. (II) or antigen presenting cells expressing (I) are useful for stimulating and/or expanding T cells so that capress (II). (II) or antigen presenting cells that express (II). (I). (II), or antigen presenting cells that express (II). (II), or antigen presenting cells that express (II) are useful for treating colon cancer in a patient by incubating CD4+ and/or CD8+ T cells that express (II), or patient with (I), (II), or antigen presenting cells that express (III) as patient with (I), (II), or and administering to the patient an effective cancer in the patient. A new composition is useful for stimulating an immune response in a patient. (I) or (II) is useful for stimulating an immune response in a patient. (I) or (II) is useful in vaccines and antibody against (III) is useful for detection, diagnosis and/ or therapy of human colon and in the design and preparation of ribozyme captured for inhibiting expression of (II) in tumour cells. ARX29475- the formal or and in the design and preparation of ribozyme captured for inhibiting expression of (II) in tumour cells. ARX29475- the formal colon adenocarcinoma-specific cDNA sequences of
                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide encoding a polypeptide comprising a portion of colon tumor protein, for detection, diagnosis and therapy of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 207; 211pp; English
                                                                                                                                                                                                                                                                                     Χu J,
                                                                                                                                07-JUN-2001; 2001WO-US018574
                                                                                                                                                                         09-JUN-2000; 2000US-0210667P. 22-NOV-2000; 2000US-0252614P.
                                                                                                                                                                                                                                                                                Meagher MJ, King GE,
                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                              WPI; 2002-098052/13
                                          WO200196389-A2
                                                                                                                                                                                                                                                                                                                                                                                                                 colon cancer.
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    Homo sapiens.
                                                                                     20-DEC-2001
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Secrist H;

Sequence 792 BP; 165 A; 218 C; 197 G; 212 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                      TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACACAA 453
                                                                 61
                                                                                   214 CAATGGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGT
                                                                                                                             TIGICAACGIGGCTACTICCTCAICGCAGCCGCGTIGIGGTCTTIGCTCTIGGTTTCC
                                                                                                                                                         274 TIGICAACGIGGGCIACTICCICAICGCAGCCGGCGIIGIGGICTIIGCICIIGGILICC
                                                                                                                                                                                         TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC
                                                                                                                                                                                                                         TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC
                                                                                                                                                                                                                                                      TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCATAA
                                                                CAAŢCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGT
                                  Gaps
                                ;
0
Score 282.8; DB 6; Length 792;
Pred. No. 8.4e-72;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                     TGGCTGAGCACTTCCCGACGTTGCTGCTGCCTGCCATCAAGAA 287
95.2%;
                Best Local Similarity 99.3
Matches 284; Conservative
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This is the nucleotide sequence of the human tumour-associated antigen

(PRAT) used in the method of the invention for stimulating cell

proliferation and screening for antegonists useful to treat or prevent

cell proliferation disorders such as cancer, and genetic defect e.g.

sickle cell anaemia. The polypeptides can be combined with a suitable

carrier in pharmaceutical compositions, and also used to screen for

antagonists, agonists, and to generate antibodies. PRAT agonists can be

carrier in pharmaceutical compositions, which can be

added to a cell to stimulate cell proliferation by increasing or

prolonging the activity of PRAT as above. The antagonists can be combined

with a suitable carrier in pharmaceutical compositions, which can be

administered to subjects to treat or prevent disorders associated with

cell proliferation, especially cancers. Antibodies specific for PRAT may

be used directly as antagonists, or indirectly as a targeting or delivery

mechanism to bring pharmaceutical agents to PRAT-expressing cells. They

expression and to monitor therapeutic interventions. The polynucleotide

chyptidisation probes, useful to detect polynucleotides or fragments

encoding PRAT, or complementary sequences, can be used to produce

chyptidisation probes, useful to detect polynucleotides or fragments

encoding PRAT, e.g. to diagnose diseases relating to polypeptide

expression or monitor PRAT regulation during therapeutic intervention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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                                                                                                                                                                                                                                                                                                                                          Human; tumour-associated antigen; PRAT; stimulation; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human tumour-associated antigen PRAT - useful for stimulating cell proliferation and screening for antagonists useful to treat or prevent cell proliferation disorders e.g. cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGT
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                                                                                                                                                                                                                                                                                                                                                                 antagonist; cancer; genetic defect; sickle cell anaemia; agonist; antibody; hybridisation; probe; ss.
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                                                                                                                                                                                                                                                           Nucleotide sequence of the human tumour-associated antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "human tumour-associated antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 933 BP; 198 A; 254 C; 236 G; 245 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 1A-1C, 54pp, English.
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                                       AAV54014 standard; cDNA; 933 BP.
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/*tag= a
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                                                                                                                                                                                        02-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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AAV54014
AAV
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                  TIGECAACGIGGGCTACTICCTCATCGCAGCCGGCGTIGTGGGCTTTGCTCTTGGTTTCC 344
                                                        TGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCATCC 181
                                                                                       404
                                                                                                                TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGGTCGCCTTGGTGTACACCATAA 241
                                                                                                                                             405 rccrccrcarcrarracraagaracaacracraracacaracacacaa 464
                                                                                                                                                                                                                                                                                                                                                                                             Human, ovarian cancer; marker, cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; brain herniations granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker; gene; ss.
TIGICAACGIGGCCTACTICCICATCGCAGCCGCGTTGTGGTCTTTGCTCTTGGTTTCC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and
                                                                          TGGCTGCTATGGTGCTAAGACTGAGAGGCAAGTGTGCCCTCGTGAGACGTTCTTCTTCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kovatis SG;
                                                                                                                                                                           TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
                                                                                                                                                                                              465. TGGCTGAGCACTTCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hoersch S, Kamatkar S, Ko
andt PJ, Sen A, Vieby PO,
, Zhao X, Glatt K;
                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding human ovarian cancer marker M328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 445-446; 481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monahan JE, Gannavarapu M, Hoersch S,
Meyers RE, Morrisey MP, Olandt PJ, S
Bast RC, Lu K, Schmandt RE, Zhao X,
                                                                                                                                                                                                                                                                              ABS76533 standard; cDNA; 1076 BP
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26-SEP-2001; 2001US-0324967P.
26-SEP-2001; 2001US-0325102P.
26-SEP-2001; 2001US-0325149P.
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2001US-0311732P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                      (first entry)
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10-AUG-2001;
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characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having an enhanced risk of developing covarian cancer markers may be used in the management and treatment cancer. The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. nontuberculous granulomateus orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disorders in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, and cancer has metastasized or is likely to metastasize, whether ovarian cancer has metastasized or is likely to metastasize, ovarian cancer has metastasized or is likely to metastasize, ovarian cancer or at risk of developing ovarian cancer. The present nucleic acid sequence encodes one of the ovarian cancer. The present nucleic acid sequence encodes one of the ovarian cancer markers described in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1076 BP; 226 A; 278 C; 283 G; 289 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.2%; Score 282.8; DB 6; ilarity 99.3%; Pred. No. 9.4e-72; Conservative 0; Mismatches 2;
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22-ANG-2001; 2001US-0314356P.
25-SEP-2001; 2001US-0352020P.
12-DEC-2001; 2001US-0341146P.
15-MAR-2002; 2002US-0362158P.
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15-JAN-2004; 2004WO-US001100
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                                                                                                                                                                                          The invention relates to newly discovered cancer markers associated with the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invention involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a prostate cancer by comparing the level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal control non-prostate cancer.

Nucleic acids of the invention as afflicted with prostate cancer.

Nucleic acids of the invention as elected in gene therapy. Sequences given in ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence cata for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
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                                                                                                                    nucleic acid molecule, useful for diagnosing or treating prostate
                                            Gorbatcheva B;
Anderson D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 1076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 282.8; DB 10; Length
Pred. No. 9.4e-72;
0; Mismatches 2; Indels
                                            Endege WO, Gannavarapu M,
onsey AM, Glatt K, Zhao X,
                                                                                                                                                                  Disclosure; SEQ ID NO 424; 99pp; English.
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                                                            Мопвеу АМ,
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              (MILL-) MILLENNIUM PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284; Conservative
                                            Monahan JE,
                                                        Kamatkar S,
                                                                                      WPI; 2003-248033/24.
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                                          Schlegel R,
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                                                            Hoersh S,
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The invention relates to a method of classifying a breast cancer patient excording to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.
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                                                                                                                                                                                                                                                                                                                       Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGT
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Pred. No. 9.4e-72;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostatic carcinoma derived DNA SEQ ID 64 #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 1191; 226pp; English
                                                                          ROSETTA INPHARMATICS LLC.
NETHERLANDS CANCER INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADR65868 standard; DNA; 1076 BP
15-JAN-2003; 2003US-00342887.
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                                                                                                                                                                                                                                                     WPI; 2004-593473/57.
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Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T; Beckmann G, Bruemmendorf T, Kinnemann H, Roepcke S;
         22-FEB-2004; 2004WO-DE000433.
                  27-FEB-2003; 2003DE-01009985.
14-MAY-2003; 2003DE-01022134.
                                     DAHL E.
ROSENTHAL A.
HERMANN K.
                                                                      Staub E;
                                                                               WPI; 2004-653386/63.
                                 HINZMANN B.
                                                   PILARSKY C.
                                                                Schmitt A, F
Xinzhong L,
10-SEP-2004;
                                                           Hinzmann B,
                                (HINZ/)
                                     (DAHL/)
(ROSE/)
(HERM/)
                                                   PILA/)
                                                                                                   agents.
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New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for specific binding Claim 1; Page 268; 1607pp; German.

This invention describes novel cytostatic polynuclectide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer. Or the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences in constraints over transcription or inhibitors of the sequences or detection substances involves a binding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of tumour cells. Inhibitors can be chosen from antisense oligonuclectides, short-interfering RNA or ribozymes; an organic molecule of molecular catamer against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide; a (monoclonal) antibody (Ab) against the polypeptide; a (monoclonal) antibody directed against Ab or any of the above derivatised with a reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polypuclectides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays. Detween normal and tumorous tissues, with (over) expression being detected by quantitative PCR. Analysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated concerpational antibody; streptavidin-conjugated horseradish percond antibody; streptavidin-conjugated horseradish perconds antibody; streptavidin-conjugated horseradish perconds antibody; streptavidin-conjugated horseradish perconds antibody; streptavidin-conjugated horseradish camples were counterstained which hemalum (blue). Mallagnant cells stained curronly but non-malignant cells only weakly. In 15 of 6 samples of proventide and nolwornide sequences used in the percondence of the polyment of the percondence of the percondence of the percondence of the percondence of t polynucleotide and polypeptide sequences used in the method of the invention.

Sequence 1076 BP; 226 A; 278 C; 283 G; 289 T; 0 U; 0 Other;

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                                                                                                 98 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGT
                                                                                                                                                                                     158 TIGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGCTCTTTGCTCTTTGGTTTCC
                                                                             2 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGT
                                                                                                                                                                                                                                                                          218 TGGGCTGCTATGGTGCTAAGACTGAGGAAGTGTGCCCTCGTGACGTTCTTCTTCATCC
                                        Gaps
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95.2%; Score 282.8; DB 13; Length 1076; 99.3%; Pred. No. 9.4e-72;
                  Pred. No. 9.4e-72;
0; Mismatches 2; Indels
                                      284; Conservative
                    Local Similarity
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This invention describes novel cytostatic polynucleotide and polypeptide sequences which can be used in a method for diagnosing prostatic cancer. Cor the risk of developing prostatic cancer. Diagnosis is based on determining over transcription or over expression of the sequences in prostatic tissue. Screening for inhibitors of the sequences or detection core substances involves a blinding assay, any compounds that bind are selected, optionally after deconvolution of mixtures. Detection of a predetermined minimum level of the reporter indicates the presence of trumour cells. Inhibitors can be chosen from antisense oligonucleotides, short-interfering RNA or ribozymes; an organic molecule of molecular veright below 5000, preferably 300, that binds to the polypeptide; an expaner against the polypeptide, a (monoclonal) antibody (Ab) against the collypeptide, preferably humanised or human; an anti-idiotype, non-human (monoclonal) antibody directed against Ab or any of the above derivatised of the reporter group, cell toxin, immunostimulatory molecules and/or radioisotope. The polymucleotides are identified in human prostatic cancer by differential expression analysis, using DNA microarrays, concer by differential expression analysis, using DNA microarrays, by quantitative POR. Manalysis of prostatic cancer samples showed that CD24 was upregulated in many of them. Sections of tissue, isolated from prostatic cancer patients, or subjects at risk, were incubated
                                    278 recreaterreariscreagerrecaecrecrererescerrecrearerecaeaa 337
182 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCATAA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
Beckmann G, Bruemmendorf T, Kinnemann H, Roepcke S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acids, and encoded proteins, from prostatic cancer tissue, useful for diagnosis, treatment and in screening for apecific binding
                                                                                                      338 TGGCTGAGCACTTCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAA 383
                                                                              242 TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA
                                                                                                                                                                                                                                                                                                                                                Human prostatic carcinoma derived DNA SEQ ID 64 #4.
                                                                                                                                                                                                                                                                                                                                                                                      human; cytostatic; diagnosis; prostatic cancer; differential expression analysis; ds.
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                                                                                                                                                                                                                      ADR66771 standard; DNA; 1076 BP
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14-MAY-2003; 2003DE-01022134.
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ROSENTHAL A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HERM/) HERMANN K.
(PILA/) PILARSKY C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004076614-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGTTGGTGTACACCATAA 241
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                                                                                                                                                                                                                                                                                                                                                                                         TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
sequentially with anti-human CD4 murine monoclonal antibodies; botinylated second antibody; streptavidin-conjugated horseradish peroxidase and then diaminobenzidine as colour former (brown). The samples were counterstained with hemalum (blue). Malignant cells stained strongly but non-malignant cells only weakly. In 15 of 63 samples of adenocarcinoma, membrane and cytoplasmic staining was very strong, and lymph node metastases were also stained. ADR65905-ADR65954 represent the polymucleotide and polypeptide sequences used in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human tumour-associated antigenic target (TAT) cDNA sequence #1895.
                                                                                                                                                                                             DB 13; Length 1076;
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                                                                                                                                                               Sequence 1076 BP; 226 A; 278 C; 283 G; 289 T; 0 U; 0 Other;
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                                                                                                                                                                                             Score 282.8; DB 13; Length
Pred. No. 9.4e-72;
0; Mismatches 2; Indels
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                                                                                                                                                                                             95.2%;
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                                                                                                                                                                                                                             Matches 284; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC. (WUTD/) WU T D. (ZHOU/) ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-534300/51.
                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                 invention.
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The present invention describes an isolated tumour-associated antigenic target (TTT) mucleic acid comprising: (a) any of 4522 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% of sequence identity to (a)-(c); or (b) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide; (6) an isolated polypeptide; (a) an amino acid sequence encoded by any of the above comprising the above polypeptide; (b) a chimaric polypeptide comprising the above polypeptide full sequence encoded by any of the above comprising the above polypeptide full sequence encoded by any of the above comprising the above polypeptide full sequence antibody that binds to the above polypeptide; (6) a chimaric polypeptide; (6) an isolated antibody that binds to the above polypeptide; (1) a process of for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (1) a comprising the above polypeptide or TAT binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide; (1) an article of manufacture comprising a container; of the growth of matter companies within the container; (12) methods of the protein; unding the protein; unding the protein; unding the protein; unding the protein; (11) an article of manufacture comprising the above protein; of a cell that expresses the above protein; (13) a method of determining the protein; of the apove protein; (13) a method of described above; (15) methods of diagnosing the presence of a protein in a sample suspected of containing the protein; and (17) a method of binding an artibody, oligopeptide to a cell that expresses the above protein; and containing the protein; and (17) a method of binding an artibody, oligopeptide to a cell that expression or activity of the above protein; ö preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a 157 121 158 frerchacerederactrecrearescasecescerrerescretrrescretraserres 217 1GGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 277 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCATAA 241 278 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCACAA 337 TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181 caarcearecearecriricreaagarerregeeceaereregeecareceare TTGTCAACGTGGGCTACTTCCTCATCGCAGCCGCTTGTGGGTCTTTGCTTTGGTTTTCC CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCGTCCAGTGCCATGCAGT Gaps ő DB 13; Length 1077; Sequence 1077 BP; 227 A; 279 C; 282 G; 289 T; 0 U; 0 Other; 242 TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287 338 TGGCTGAGCACTTCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAA 383 Score 282.8; DB 13; Length Pred. No. 9.4e-72; 0; Mismatches 2; Indels human TAT cDNA sequence from the present invention. tch 95.2%; al Similarity 99.3%; 284; Conservative ~ 98 62 122 218 Query Match Best Local S 182 Matches ઠે 요 Š a Š a ઠ 셤 ò

ABS76532 standard; cDNA; 1154 BP ABS76532; RESULT 13 ABS76532 #####

(first entry) 11-DEC-2002

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Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; brain herniation; comective tissue disorder; heart disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker; gene; ss.
          cDNA encoding human ovarian cancer marker M327.
                                                                                                                                                                        14-MAR-2001; 2001US-0276025P.
14-MAR-2001; 2001US-0276026P.
10-AUG-2001; 2001US-0311732P.
19-SEP-2001; 2001US-0323580P.
26-SEP-2001; 2001US-032457P.
26-SEP-2001; 2001US-0325102P.
                                                                                                                                                        14-MAR-2002; 2002WO-US007826
                                                                                                                                                                                                                                 26-SEP-2001; 2001US-0325149P
                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC
                                                                                                                   WO200271928-A2
                                                                                                    Homo sapiens
                                                                                                                                       19-SEP-2002
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Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Kovatis SG, Meyers RE, Morrisey MP, Olandt PJ, Sen A, Vieby PO, Mills GB; Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;

WPI; 2002-723277/78. P-PSDB; ABG96433. Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and non cancer patient. ď from

Disclosure; Page 444-445; 481pp; English

The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression of the marker in a patient sample and the normal level of expression of the marker in a patient sample and the normal level of expression of the marker in selected from 363 cancer markers described in the comparing the marker is selected from 363 cancer markers described in the constraint or selected from 163 cancer. The method may also be of characterising cancer, in detecting the presence of cancer as early as particular use with patients having an enhanced risk of developing covarian cancer (e.g. patients having an enhanced risk of developing covarian and central nervous system disorders (e.g. brain et.g. barcerial ocdema, hydrocephalus or brain herniations), conficular disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart cused in assessing the histological type of neoplasm associated with covarian cancer, monitoring the progression of ovarian cancer, determining coloring and methods may also be coloring and methods may also be conserved to the season of the coloring of coloring and methods was entered to the coloring the progression of ovarian cancer, determining coloring and methods may also be coloring and methods may also be coloring the progression of ovarian cancer, menitoring the progression of ovarian cancer and the coloring the progre selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present nucleic acid invention

Sequence 1154 BP; 307 A; 309 C; 255 G; 283 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the cancerous state of prostate cells. Also disclosed is a method of assessing whether a patient is afflicted with prostate cancer. The method of the invantion involves assessing whether a patient is afflicted with prostate cancer by comparing the level of expression of a marker in a patient sample and the normal level of expression of the marker in a control non-prostate cancer sample, where a significant increase in the level of expression of the marker in the patient sample and the normal level indicates that the patient is afflicted with prostate cancer. Nucleic acids of the invention are useful for diagnosing or treating prostate cancer, and may be useful in gene therapy. Sequences given in
                                                 61
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                                                                       221 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCGTCGTCGTGCCATGCAGT
                                                                                                                62 TIGICAACGIGGGCTACTICCICAICGCAGCCGGCGTIGIGGICTIIGCICTIGGITITCC
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                 Indels
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att K, Zhao X,
 Pred. No. 9.7e-72;
0; Mismatches 2;
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2001US-0325020P.
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05-MAR-2002; 2002US-0362158P.
   99.3%;
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                 284; Conservative
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Local Similarity
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25-SEP-2001;
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Hoersh S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, differential expression; cancer; angiogenic disorder;
fibroric disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
inflammatory disease; autoimmune disease;
retinal neovascularistaion syndrome; scarring; uterine fibroid;
detection; disagnosis; prognosis; drug screening; drug targeting;
wound healing; contraception; cytostatic; cardiant; immunomodulatory;
vulnerary; gene therapy; vaccine; gene; ss.
ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                       CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGT
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                                                                                                      0; Gaps
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                                                                              Score 282.8; DB 10; Length 1154;
Pred. No. 9.7e-72;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                             461 TGGCTGACACTTCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAA 506
                                                                                                                                                                                                                                                                                                                  242 TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
                                                         Sequence 1154 BP; 307 A; 309 C; 255 G; 283 T; 0 U; 0 Other;
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29-NOV-2001; 2001US-0334393P.
03-DEC-2001; 2001US-0334393P.
14-DEC-2001; 2001US-0340376P.
10-JAN-2002; 2002US-0347211P.
10-JAN-2002; 2002US-034731P.
13-FEB-2002; 2002US-0355250P.
20-FEB-2002; 2002US-0355714P.
29-MAR-2002; 2002US-0359077P.
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12-APR-2002; 2002US-037246P.
05-UTM-2002; 2002US-0386614P.
16-UTL-2002; 2002US-0396839P.
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                                                                              Query Match
Best Local Similarity 99.3%;
Matches 284; Conservative
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention or by detecting a polypeptide of the invention or by detecting a polypeptide of the invention, use of such antibodies for drug targeting; an uncleic acid of the invention; antibodies which specifically bind a polypeptide of fereening for medulators of earthing; and methods of screening for medulators of earthing; and nucleic acids. The nucleic acids, polypeptides, and nucleic acids are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, attended also be useful in wound healing and in contracetion. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278
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Murray R, Watson SR, Wilson KE, Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.2%; Score 282.8; DB 99.3%; Pred. No. 1e-71; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; SEQ ID NO 603; 1385pp; English.
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                                                                                                                                                 (EOSB-) EOS BIOTECHNOLOGY INC.
22-JUL-2002; 2002US-0397775P.
22-JUL-2002; 2002US-0397845P.
09-SEP-2002; 2002US-0409450P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 284; Conservative
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Homo sapi 70 human

Sequence 70 human

AX106213 AX106330 AX200481 AX200481 BX26713 BX07259 BC013404 BD19562 CQ775562 CQ775562 CQ775562 CQ775597 AX322607 AX32607 BD19608 BD197338 AX193317 AX193317 BX103338

Sequence

Sequence

Sequence Sequence Sequence

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Sequence Method of

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Sequence Secreted

Sequence Sequence

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TTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGTCTTTGCTCTTGGTTTC 120
                                                                                                                                                                                                                                                                                         unidentified
unclassified.
1 (bases 1 to 297)
1 (bases 1 to 297)
DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
PATENT: WO 9823775-A 1 04-JUN-1998;
DEUTSCHES KREBSFORSCH (DE); NEES MATTHIAS (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCGTCCTCCAGTGCCAG
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100.0%; Pred. No. 2.2e-68;
iive 0; Mismatches 0;
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Sequence 1 from Patent WO9823775.
A91802
A91802.1 GI:6740681
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BD228312
CQ414131
CQ491480
BD190734
AX099394
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AX079459 Sequence
AX19319 Sequence
AX19319 Sequence
BD070552 Novel hum
AF13425 Homo sapi
CQ719831 Sequence
AF065388 Homo sapi
CQ719831 Compounds
BD069078 Polynucle
BD069078 Polynucle
BD642023 Compounds
AR277206 Sequence
AR378230 Sequence
AR378230 Sequence
AR3982237 Sequence
AR39962 Sequence
                                                August 27, 2005, 07:03:53 ; Search time 1577.61 Seconds (without alignments) 9122.136 Million cell updates/sec
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      GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                    4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
                                   nucleic search, using sw model
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BD023236
AX19459
AX193458
AX319319
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AF133425
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PAT 22-JAN-2000

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Length 297; 0; Indels 9

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RESULT 2 BD023236 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOUNCE ORGANISM

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REFERENCE AUTHORS TITLE JOURNAL

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 TGGGCTGCTATGGTGCTAAGACTGAGAAGTGTGCCCTCGTGACGTTCTTCTTCATCC
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Compounds for immunotherapy and diagnosis of colon cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 282.8; DB 6
Pred. No. 1.4e-64;
0; Mismatches 2
                                                                                                                                                                                                                             Baker, K.P., Goddard, A. and Wood, W.I.
Human polypeptides and methods for the
Patent: WO 0107611-A 203 01-FEB-2001;
Genencech, Inc. (US)
                         DNA
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Patent: WO 0149716-A 1025 12-JUL-2001;
CORIXA CORPORATION (US)
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Sequence 1025 from Patent W00149716.
AX193458.1 GI:15211409
                         AX079459 513 bp 1
Sequence 203 from Patent WO0107611.

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/db_xref="taxon:9606"
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Best Local Similarity 99.3%;
Matches 284; Conservative
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DNA for evaluating progress potential of cervical diseases
Patent: JP 2001504703-A 1 10-APR-2001,
DEUTSCHES KRESPORSCHUNGSZENTRUM STIFTUNG DES EFFENTLICHEN RECHTS
PN JP 2001504703-A/1
PD 10-APR-2001
PP 12-NOV-1996 DE 19649207.6
PR 27-NOV-1996 DE 19649207.6
PR 27-NOV-1996 DE 19649207.6
PR 27-NOV-1996 DE 19649207.6
PC C12N15/09, C07K14/00, C07K16/00, C12P21/02, C12Q1/68, C12Q1/70, PC G01N13/574.

C12N15/00
CC Strandedness: Double;
CC Strandedness: Double;
CC Strandedness: Double;
FH Key
FT CDS
                                                                                                                                                                                                                                                                                         BD023236 297 bp DNA linear PAT 27-AUG-2002 DNA for evaluating progress potential of cervical diseases. BD023236
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CTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCTCGTGACGTTCTTCTTCATC 180
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                                                               CTCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCATA 240
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 297)
Durust,M. and Ness,M.
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100.0%; Score 297; DB 6;
Best Local Similarity 100.0%; Pred. No. 2.2e-68;
Matches 297; Conservative 0; Mismatches 0;

    .297
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JP 2001504703-A/1.
Homo sapiens (human)
Homo sapiens
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Pule, K.L., Ni, J., Liu, D., Morahan, G. and Wright, M.D.
                                                                                        AUTHORS

I (Dases 1 to 933)

AUTHORS

Hillman, J.L. and Goli, S.K.

TITLE

Novel human tumor-associated antigen
JOURNAL

INCTTE PHARMACEUTICALS INC

OS Unidentified

Ph 18-SEP-2001;

Ph 28-REB-1997 US 08/808148

Ph 28-FEB-1997 US 08/808148

Ph JENNIFER L HILLMAN, SURYA K GOLI

PC C12N15/12, CO7X14/705, A61K38/12, CO7X16/28, GOIN33/50 CC

Strandedness: Single;

CC Topology: Linear;

CC Topology: Linear;

CC Topology: Linear;

CC Topology: Linear;

FH Key

FT Source
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                                           linear
                                           552 933 bp DNA human tumor-associated antigen.
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   RESULT 6
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                         335 TGGCTGAGCACTTCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAA 290
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0; Mismatches 2; Indels
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CORIXA CORPORATION (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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 98.38;
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Homo sapiens
Best Local Similarity 99.33
Matches 284; Conservative
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/translation="MCCFSFIKTMMILFNILLIFLCGAALLAVGIWVSIDGASFLKIFG
PLSSSAMOFVNVYFLIAAGVVVFRLGFLGGYGAKTESKCALVTFFFILLIFFTAEVA
AVVALVYTTYTAAEHPITLIVYVAIKKOYGSQEDFTQVWNTTWKGLKCGFTNYTDFED
SPYFKENSAFPFFCCTNYTDATATGTTEQKAHDQKVEGCFNQLLYDIRTNAVTVGGV
AAGIGGLELAAMIVSMYLYCNLQ"
                                                                                                                                      l. .726
| gene="TSPAN-1"
| note="tetraepanin; transmembrane 4 super family; Tspan-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT 03-FEB-2004
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 282.8; DB 9; Length 1076; Pred. No. 1.4e-64; 0; Mismatches 2; Indels 0;
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Patent: WO 02068579-A 5765 06-SEP-2002;
                                                                                                                                                                                                 /codon_start=1
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/protein_id="AAC6914.1"
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Location/Qualifiers
1. 1007
/organism="Homo sapiens"
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/db_xref="taxon:9606"
                                     organism="Homo sapiens"
                                                      /mol_type="mRNA"
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location/Qualifiers
                                                                                                                   gene="TSPAN-1"
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/db_xref="G1:6434904"

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Homo sapiens tetraspan TM4SF (TSPAN-1) mRNA, complete cds.
AF054838
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Todd.S.C., Doctor, V.S. and Levy, S.
Direct Submission
Submitted (19-MAR-1998) Medicine, Stanford, 300 Pasteur, Stanford,
CA 94305-5115, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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1 (bases 1 to 1076)

Todd,S.C., Doctor,V.S. and Levy,S.
Sequences and expression of six new members of the tetraspanin/TM4SF family
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                                   2 (bases 1 to 1044)
Puls, K.L., Ni,J., Liu,D. and Wright,M.D.
Direct Submission
Submitted (08-MAR-1999) Immunology, The Walter & Eliza Hall
Institute, Royal Parade, Parkville, Victoria 3031, Australia
Location/Qualifiers
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  molecular characterization of four tetraspanins
                                                                                                                                                                                                                                                                'note="transmembrane 4 superfamily member"
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Biochim. Biophys. Acta 1399 (1), 101-104 (1998)
98390278
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                                                                                                                                                           1. .1044
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124. .849
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PAT 27-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OS Unidentified
PN JP 2001509679-A/4
PD JP 201509679-A/4
PD 24-JUL-2001
PF 21-JAN-1998 JP 1998534602
PR 21-JAN-1998 JP 60/034204, 21-JAN-1997 US 60/034205 PI
JIAN NI, FEINER L GENTZ, CRAIG A ROSEN
PC C12N15/12, C12N15/85, C12N5/10, C07K14/705, C07K16/28, C12Q1/68, A61K38/17,
279 TIGICARCAGGGGTACTTCCTCATCGCAGCGGGTTCTGGGTTTGCTCTTGGTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 TIGICARCEGGGCTACTICCTCATCGCAGCCGGCGTTGTGGCTTTGCTCTTGGTTTCC
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Polynucleotides and polypeptides encoding receptors FH
Location/Qualifiers
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1 (bases 1 to 1288)

Ni,J., Gentz,R.L. and Rosen,C.A.

TILE Polynuclectides and polypeptides encodin.

URNAL Patent: JP 2001509679-A 4 24-JUL-2001;

NT OS Unidentified

NT JP 2001509679-A/4

PD 24-JUL-2001

PP 21-JAN
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Matches 284; Conservative
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APYFKENSAFPFFCCMDNVTNTANETCTKQKAHDQKVEGCFNQLLYDIRTNAVTVGGV
AAGIGGLELAAMIVSMYLYCNLQ
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                                                                                                                  TIGICAACGIGGGCTACTICCICAICGCAGCCGGCGTTGGTGGTCTTTGCTCTTGGTTTCC 121
                                                                                                                                    TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
                                                                                                                                                                                                                218 TGGGCTGCTATGGTGCTAAGACTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 277
                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                          Submitted (14-MAY-1998) INSERM U268, 14 av Paul Vaillant Couturier,
Villejuif 94807, France
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                                          61
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                    182 TCCTCCTCATCTTCATTGCTGAGGTTGCTGCTGCTGGTCGCCTTGGTGTACACCATAA
                                                                          98 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCCACTGTCGTCCAGTGCCAGT
                                        CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCAGT
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    Gaps
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                                                                                                                                                                                                                                                                                                                                                                    338 TGGCTGAGCACTTCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAA 383
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Homo sapiens tetraspan NET-1 mRNA, complete cds.
  Indels
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Serru, V., Dessen, P., Boucheix, C. and Rubinstein,
Sequence and expression of seven new tetraspans
Biochim. Biophys. Acta 1478 (1), 159-163 (2000)
  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TM4SF"
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Rubinstein, E., Serru, V. and Boucheix, C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to Tspan-1;
/codon_start=1
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. 1278
/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE ID 511239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product="tetraspan NET-1"
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Matches 284; Conservative
  284; Conservative
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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PR 14-JUL-1998 US 09/115453,14-JUL-1998 US 09/116134 PR

13-SEP-1998 US 09/15982,23-SEP-1998 US 09/132149 PR

15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR

15-JAN-1999 US 09/28280,15-JAN-1999 US 09/232149 PR

15-JAN-1999 US 09/282846

PI DAVIN CLIFFORD DILLON, SUGAN LOUISE HARLOCKER, JIANG YUQIU, PI

JIANGCHUN XU.

PC CLINIS/09, A61K38/00, A61K39/00, A61K39/395, CO7K14/47, CO7K16/30, PC CLINIS/09, A61K38/00, A61K39/00, A61K39/395, CO7K14/47, CO7K16/30, PC CLINIS/09, CLINIS/00, PC CLINIS/00, A61K37/02, PC CLINIS/00, CC Compounds for immunotherapy and diagnosis of prostate cancer and methods

CC Compounds for immunotherapy and diagnosis of prostate cancer and methods

CC Compounds for immunotherapy and diagnosis of prostate cancer and methods

CC C Compounds for immunotherapy and Correct and Correct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1289) Entheria; Primates; Catarrhini; Hominidae; Homo. Dillon, D.C., Harlocker, S.L., Yuqiu, J., Xu, J. and Mitcham, J.L. Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use Patent: JP 2002520054-A 110 09-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTGGTCGCCTTGGTGTACACCATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
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AR237206.1 GI:27281864
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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BD242023.1 GI:330517 JP 2002520054-A/110. Homo sapiens (human)
                                                                                                                             Homo sapiens
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BD242023
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Polynucleotides and polypeptides encoding receptors FH
Location/Qualifiers
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95.2%; Score 282.8; DB 6; Length 1288;
Best Local Similarity 99.3%; Pred. No. 1.4e-64;
Matches 284; Conservative 0; Mismatches 2; Indels 0;
TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 2001509679-A/21.
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Xa,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Yados,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate
                                                                                                                                                                                                                                                                                                                                          220 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGGTCCAGTGCCATGCAGT
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                               Unclassified.
Unclassified.

(bases 1 to 1289)
Xu,J., Dillon,D.C. and Mitcham,J.L.
Compounds for immunotherapy of prostate cancer and methods for their use
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Patent: US 6512094-A 111 28-JAN-2003;
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                                                                                                                    Patent: US 6465611-A 111 15-OCT-2002;
Location/Qualifiers
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score greater than or equal to the score of the result being printed,
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282.8	95.2	584	ស	BP263144	BP263144	BP263144
282.8	95.2	585	Ŋ	BP331321	BP331321	BP331321
38 282.8	95.2	585	9	CB216655	CB216655	NISC ng07
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282.8	95.2	613	4	BM828457	BM828457	K-EST0101
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#### ALIGNMENTS

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	Site 2: Sfil (ggccgcctcggcc); Library is oligo-dT primed and directionally cloned. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGCGACATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.30 C, or G and N = A, C, G, or T). Average insert size 1.30 C, ATTGTAGAGGCGGCGACATG-GT(30)BN-3' (where B = A, C, G,

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 518)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
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laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."
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by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
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Korea Research Institute of Bioscience & Biotechnology
Sceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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95.4%; Score 283.2; DB 7;
Best Local Similarity 99.0%; Pred. No. 2.6e-68;
Matches 285; Conservative 0; Mismatches 3;
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Unpublished (2002)
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Email! yongsung@mail.kribb.re.kr
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EST25750 human nasopharynx Homo sapiens CDNA, mRNA sequence.
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                                                                                                                                                                  285 TTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGTCTTTGCTCTTGGTTTTCC
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/clone_lib="human nasopharynx"
/note="ESFs generated from a normal nasopharynx cDNA
library from southern Chinese"
                                     Gaps
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                                   2; Indels
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651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Score 282.8; DB 6;
Pred. No. 3.1e-68;
0; Mismatches 2;
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/organism="Homo sapiens"
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Location/Qualifiers
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CD709223.1 GI:32239853
 95.2%;
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llarity 99.3%;
Conservative
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Contact: YiXin Zeng
Cancer Center
 Query Match
Best Local Similarity 99.3
Matches 284; Conservative
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BM819711.1 GI:19176124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
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//lab host="Toplop""
//lab host="Toplop"
//clone lib="SlaN669761"
//clone lib="SlaN669761"
//note="Organ: Stomach; Vector: pCNS; Site_l: EcoRI;
Site_2: Noti; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The GT-tailed vector was adjusted to have about 60nt. The CDNA vector was circularized with B. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Toplof* by electroporation method. The CDNA libraries constructed by this method are full-length enriched CDNA library."
                                                                                                                                                                                                                                                                                                                              BM819747 542 bp mRNA linear EST 06-MAR-2002
K-EST0087909 S18N669761 Homo sapiens cDNA clone S18N669761-20-G10
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1 (bases 1 to 542)
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1 (bases 1 to 542)
1 (bases 2 to 542)
1 (bases 3 to 542)
1 (bases 3 to 542)
2 (bh.K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
276 TGGCTGCTATGGTGCTAAGACTGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 335
                                                                        TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCATAA 241
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Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Email: yongsung@mail.kribb.re.kr
Plate: 20 row: G column: 10
High quality sequence stop: 542.
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                                                                                                                                                               242 TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
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Unpublished (2002)
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/mol_type="mRNA"
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/clone="S18N669761-20-G10"
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/lab host="Top10F'"
//lab host="Top10F'"
/clone lib="618N669761"
/clone lib="618N669761"
/clone lib="618N669761"
/clone lib="618N669761"
/site 2: Not1; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intect mRNA was ligated with DNA-RNA linker including EGOR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with B. coll DNA ligase after digestion of ECONI which site is also included in vector. An RNA strand converted to a DNA strand by Okayam-Berg method. The
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1 (bases 1 to 543)
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(kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J. M., Park, H.S., Kim, S. and
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K-EST0087869 S18N669761 HOmo sapiens CDNA clone S18N669761-20-D06
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266 TIGICAACGIGGGCIACTICCICAICGCAGCCGGCGTIGGGTCTTIGCTCTIGGTTCC 325
                                                                                                                         TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
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21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kin YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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/db_xref="taxon:9606"
/clone="$18N669761-20-D06"
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/organism="Homo sapiens"
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Plate: 20 row: D column: 06
High quality sequence stop: 543.
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                                   TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCATAA 241
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                                                                                                                                                                                                                                                                                                                                                                                                                     366 TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 425
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1 (Dases 1 to 546)
Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng, Y.-X.
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/Lolone_Ilb="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"
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EST16536 human nasopharynx Homo sapiens CDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGCTGAGCACTTCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAA 531
                                   Indels
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      Pred. No. 3.1e-68;
0; Mismatches 2;
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email yxzeng@gzsums.edu.cn.
Location/Qualifiers
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651 DöngFeng Road East,
Tel: å6-1380-9770-743
Fax: å6-20-8775-4506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD700012
CD700012.1 GI:32229841
Best Local Similarity 99.3%;
Matches 284; Conservative
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Contact: YiXin Zeng
Cancef Center
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AUTHORS
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COMMENT
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Homo saptens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (Labasea 1 to 549)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Mational Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong Library

CDNA Library Preparation: Ling Hong Library

COLOR distribution: MGC Clone distribution information can be

found through the I.M.A.G.E. Consortium/LiNt at: image.lln.gov

Plate: LiCMB: Towis a column: 12

High quality sequence stop: 549.

Location/Qualifiers

J. 549

J. 540

J. 549

J. 540

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evoy4294F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959379 5',
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
1 (bases I to 559)
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                                           351 TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCTTCTTC 410
                                                                                                                                                                                     411 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGGTCGCCTTGGTGTACACCACAA 470
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKPZ); Bmail s.wiemann@dkfz- heidelberg.de;
sequenced by GRF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
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/note="Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No 81 sequence available.
This clone (DKPZp686E20218) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Hewbnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                             182 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC
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Pred. No. 3.1e-68;
0; Mismatches 2;
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/mol_type="mRNA"
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/clone lib="SlNN669761"
/clone lib="SlNN669761"
/clone lib="SlNN669761"
/clone lib="SlNN669761"
/inote="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand CDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which strend by Okayama-Berg method. The converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of converted coll Toplof* by electroporation method. The cDNA libraries constructed by this method are full-length enriched CDNA library."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 554)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.B., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                                                                                             BM819756 554 bp mRNA linear EST 06-MAR-2002
K-EST0087919 S18N669761 Homo sapiens CDNA clone S18N669761-20-H08
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386 TCCTCCTCATCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCACAA 445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Korea Research Institute of Bioscience & Biotechnology 52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Email: yongsung@mail.kribb.re.kr plate: 20 row: H column: 08 Plate: 20 row: H column: 08 High quality sequence stop: 554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 282.8; DB 4; Length 554;
Pred. No. 3.1e-68;
0; Mismatches 2; Indels 0;
                                                                 242 TGGCTGACCATTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
                                                                                                         21C Frontier Korean EST Project 2001
Unpublished (2002)
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Genome Research Center
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Matches 284; Conservative
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/lab host="Toplop""
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//clone lib="SiBN669761"
//clone lib="SiBN669761"
//clone lib="SiBN669761"
//site_2: Not1; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECOR I site by treatment of T4 RNA ligase and the first strand cDNA was synthhesized from oligo dT-selected mRNA by priming with dT-tailed vector. The CT-tailed vector was adjusted to have about 60nt. The CDNA vector was circularized with E. coli DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of convertent cells E. coli Toplof' by electroporation method. The CDNA libraries constructed by this method are full-length enriched CDNA library."
                                                                                                                                                                                                                                                     BM819724 566 bp mRNA linear EST 06-MAR-2002
K-EST0087883 S18N669761 Homo sapiens CDNA clone S18N669761-20-E08
5', mRNA sequence.
BM819724
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             413 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCACAA 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 566) (Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.
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Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-866-4470
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Pred. No. 3.1e-68;
0; Mismatches 2; Indels 0;
                                                                242 TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
                                                                                               473 TGGCTGAGCACTTCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAA 518
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Unpublished (2002)
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/db_xref="taxon:9606"
/clone="S18N669761-20-E08"
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/organism="Homo sapiens"
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Plate: 20 row: E column: 08
High quality sequence stop: 566.
Location/Qualifiers
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Best Local Similarity 99.3%;
Matches 284; Conservative
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim, Y.S.
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/lab_host="IMAGE:4608394"
/lab_host="DH10B (T1 phage-resistant)"
/clone=lib="NIH MGC 75"
/clone=lib="NIH MGC 75"
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
Sfil (ggccgctcggcc); Site_2: Sfil (ggccattatggcc); S
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCCATTATGGCC'3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

B. (Lassea I to S64)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Fland through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop; 560.

Location/Qualifiers

1.05
                                                                                                                                                                                                                                                                            BG428609 564 bp mRNA linear EST 14-MAR-2001
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293 Trerchacereceractrecrearedeaceaceacerrerecrerrecrerregimes 352
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                                                                                   TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
                                                                                                                        474 TGGCTGAGCACTTCCTGACGTTGCTGGTAGTGCCTGCCATCAAGAA 519
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/mol_type="mRNA"
/db_xref="taxon:9606"
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             TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGGTCGCCTTGGTGTACACCATAA 241
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Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
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                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCCTCGTGACGTTCTTCTTCATCC
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95.2%; Score 282.8; DB 5; Length
Best Local Similarity 99.3%; Pred. No. 3.1e-68;
Matches 284; Conservative 0; Mismatches 2; Indels
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RESULT 13 BP262643

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

E. (Dases I to 568)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizuki, Y., Yamashita, R., and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711–1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
1 Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
Lorganism=Homo sapiens"
568 bp mRNA linear EST 16-SEP-2004
BP262643 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HSI07585, mRNA sequence.
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F.EST0087855 S18N669761 Homo sapiens CDNA clone S18N669761-20-C03
EM819701
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1. (Dases 1 to 571)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.B., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and 21C Frontier Korean EST Project 2001
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/db zref="taxon:9606"
/clone="MS107585"
/tissue type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"
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//db host="ToploF" |
//db host="Dogan: Stomach; Vector: pCNS; Site_1: EcoRI;
//dloe="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mANA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand CDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The CDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which strand by Okaayama-Berg method. The converted to a DNA strand by Okaayama-Berg method. The obtained cDNA vectors were used for transformation of converted to a DNA strand by Okaayama-Berg method. The CDNA libraries constructed by this method are full-length enriched CDNA library."
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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           Contact: Kim YS.

Contact: Kim YS.

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Tel: +82-42-860-4470
Fax: +82-44-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 20 row: C column: 03
High quality sequence stop: 571.
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                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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Homo sapiens
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Matches 284; Conserv
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 571)
S Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Email: ysuzukiaina.u-tokyo.ac.jp.
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Best Local Similarity 99.3
Matches 284; Conservative
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Sat Aug 27 12:11:20 2005

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Sequence 1, Appli
Sequence 203, App
Sequence 1025, Ap
Sequence 1025, Ap
Sequence 361, App
Sequence 361, App
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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4 US-10-052-217-1025

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US-09-833-263-1025

3 US-10-025-380-1025

US-09-878-134-361

9 US-10-775-920-132
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Maximum Match 100%
Listing first 45 summaries
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Sequence 325, App Sequence 424, App Sequence 1191, Ap Sequence 1191, Ap Sequence 136, App Sequence 422, App Sequence 603, App Sequence 603, App	Sequence 4, Appli Sequence 50, Appl Sequence 50, Appl Sequence 111, App Sequence 113, App Sequence 114, Appl Sequence 114, Appl Sequence 115, App Sequence 117, Appl Sequence 117, Appl Sequence 118, Appl Sequence 118, Appl Sequence 119, Appl Sequence 119, Appl Sequence 119, Appl Sequence 111, Appl Sequence 114, Appl Sequence 114, Appl Sequence 114, Appl Sequence 114, Appl	
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                                                                                                                                                                                                          Query Match 100.0%; Score 297; DB 13; Best Local Similarity 100.0%; Pred. No. 1.3e-84; Matches 297; Conservative 0; Mismatches 0;
                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
US-10-079-954-1
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) LOCATION: 618 7
; OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 99.3%;
Matches 284; Conservative
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ORGANISM: Homo sapiens
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                                                                          61 TTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGTCTTTGCTCTTGGTTTT 120
                                                                                                                                                                      CTGGGCTGCTATGGTGCTAAGACTGAGGAAGTGTGCCCTCGTGACGTTCTTCTTCATC 180
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                                               61 TITGICAACGIGGGCTACTICCTCATCGCAGCCGGCGTIGIGGTCTTTGCTCTTGGTTTC 120
                                                                                                                                             CTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATC 180
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GCAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAG 60
                                                                                                                                                                                                                                                                                                                                       241 ATGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAAGATTATGGTT 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 203, Application US/10052283
; Sequence 203, Application US/10052283
; Publication No. US20030064379A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Goddard, Audrey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND METHOD OF USE THEREOF
; FILE REFERENCE: P2751RIC.
; CURRENT APPLICATION NUMBER: US/10/052,283
; CURRENT PILING DATE: 2002-01-15
; PRIOR FILING DATE: 2000-07-21
; PRIOR FILING DATE: 1999-07-26
; NUMBER OF SEQ ID NOS: 564
; SEQ ID NOS: 564
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Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 TYPE: DNA
CORGANISM: Homo Sapien
US-10-052-283-203
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US-09-922-217-1025/c
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Sequence 1025, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aliun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Madher, Madelene J.
; APPLICANT: Madher, Madelene J.
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE; TITLE REPERENCE: 21011.471C1.2
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1025
; LENGTH: 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        395 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTCGCCTTGGTGTACACCACAA 336
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APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Yudiu
APPLICANT: Smith, Carole Lynn
APPLICANT: Wing, Gordon E.
APPLICANT: Carole Lynn
APPLICANT: Carole Lynn
APPLICANT: Carole Lynn
APPLICANT: Carole Compounds FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT FAILE DADE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1025
LENGTH: 635
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Pred. No. 5.4e-80;
0; Mismatches 2; Indels 0
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ORGANISM: Homo sapien
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395 TCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGGTCGCCTTGGTGTACACCACAA 336
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                                                                                                                           62 INGICAACGIGGGCIACTICCTCATCGCAGCCGGCGTIGIGGICTTIGCTCTTGGTTTCC
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                 2 CAAICGAIGGGGCAICCITICIGAAGAICTICGGGCCACTGICGICCAGIGCCAIGCAGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Meagher. Madeleine Joy
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: SCIGHE, Heather
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF COLON CANCER
FILE REPERENCE: 210121.532
CURRENT APPLICATION NUMBER: US/09/878,134
CURRENT FILING DATE: 2001-06-07
NUMBER OF SEQ ID NOS: 377
SEQ ID NO 361
LENGTH: 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 99.3
Matches 284; Conservative
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CORGANISM: Homo sapiens
US-09-878-134-361
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kodes, Michael J.
APPLICANT: Secriet, Heather
APPLICANT: Stick, John A.
APPLICANT: Smith, Carole L.
APPLICANT: Smith, Carole L.
APPLICANT: Smith, Carole L.
APPLICANT: Smith, Carole L.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Carber, Darrick
AP
                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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95.2%; Score 282.8; DB 13; Length 635;
Best Local Similarity 99.3%; Pred. No. 5.4e-80;
Matches 284; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                   Query Match 95.2%; Score 282.8; DB 9; Length 635; Best Local Similarity 99.3%; Pred. No. 5.4e-80; Matches 284; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGCTGAGCACTTCCCGACGTTGCTGGTAGTGCCTGCCATCAAGAA 287
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(635)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-263-1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
: LOCATION: 618
; OTHER INFORMATION: n = A,T,C or G
US-10-025-380-1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-025-380-1025/c
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US-10-775-920-132 Sequence 132, Application US/10775920 Publication No. US20040175744A1 GENERAL INFORMATION:

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Sequence 424, Application US/10205823

Sequence 424, Application US/10205823

Publication No. US20030108963A1

Sequence 424, Application US/10205823

Publication No. US20030108963A1

APPLICANT: Schlegel, Robert

APPLICANT: Monahan, John E.

APPLICANT: APPLICANT: Bella

APPLICANT: Gorbatcheva, Bella

APPLICANT: Gorbatcheva, Bella

APPLICANT: Monsey, Angela M.

APPLICANT: Monsey, Angela M.

APPLICANT: Anderson, Dustin

APPLICANT: Anderson, Dustin

APPLICANT: Anderson, Dustin

TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

TITLE OF INVENTION: THERAPY OF PROSTATE CANCER

TITLE OF INVENTION WHERE: 60/314,356

PRIOR APPLICATION NUMBER: 60/314,356

PRIOR APPLICATION NUMBER: 60/314,366

PRIOR APPLICATION NUMBER: 60/314,366

PRIOR FILING DATE: 2001-07-25

PRIOR APPLICATION NUMBER: 60/314,746

PRIOR FILING DATE: 2001-12-12

PRIOR PILING DATE: 2001-12-12

PRIOR PILING DATE: 2001-12-12

PRIOR PILING DATE: 2001-12-12

PRIOR PILING DATE: 2001-12-12
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95.2%; Score 282.8; DB 1.
Best Local Similarity 99.3%; Pred. No. 6.3e-80;
Matches 284; Conservative 0; Mismatches 2
     PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/324,967

PRIOR FILING DATE: 2001/09/26

PRIOR PILING DATE: 2001/09/26

PRIOR PILING DATE: 2001-03-10

PRIOR PILING DATE: 2001-09-26

PRIOR PILING DATE: 2001-09-26

PRIOR PILING DATE: 2001-09-26

PRIOR PILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 363

SOFTWARE: PEASESEQ for Windows Version 4.0

SOFTWARE: 1076
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo sapiens
US-10-097-340-325
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APPLICANT: Mergen Ltd
TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
TITLE OF INVENTION: 10 CERTAIN CANCERS
FILE REFERENCE: Mergen - 0010B
CURRENT APPLICATION NUMBER: US/10/775,920
PRIOR PILING DATE: 2004-02-10
PRIOR FILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 385
SOFTWARE: PatentIn version 3.2
SEQ ID NO 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 325, Application US/10097340

Sequence 325, Application US/10097340

Publication No. US20030087250A1

GENERAL INFORMATION:

APPLICANT: Sebastian HODERCH
APPLICANT: Steve G. KOVATS

APPLICANT: Steve G. KOVATS

APPLICANT: APPLICANT: Michael MORRISES

APPLICANT: Machael MORRISES

APPLICANT: Rosemarie SCHWANDT

APPLICANT: Rosemarie SCHWANDT

APPLICANT: Karen LU

APPLICANT: Karen LU

APPLICANT: Karen LU

APPLICANT: Karen SCHWANDT

APPLICANT: Karen GLATT

ITILE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,

ITILE OF INVENTION: Nucleic Acid Molecules and Proteins Cancer

FILE REPERENCE: MIL O 30

CURRENT APPLICATION NUMBER: 60/226,025

PRIOR APPLICATION NUMBER: 60/225,149

PRIOR PILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/276,026
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Best Local Similarity 99.3
Matches 284; Conservative
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; ORGANISM: Homo sapiens
US-10-775-920-132
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                                       TGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATCC 181
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US-10-775-920-136
; Sequence 136, Application US/10775920
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CORGANISM: Homo sapiens
US-10-342-887-1191
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                                                                                                                                                             Query Match 95.2%; Score 282.8; DB 15; Length 1076; Best Local Similarity 99.3%; Pred. No. 6.3e-80; Matches 284; Conservative 0; Mismatches 2; Indels 0;
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               NUMBER OF SEQ ID NOS: 455
SOFTWARE: PSSLSEQ for Windows Version 4.0
SEQ ID NO 424
LENGTH: 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1191, Application US/10172118
Publication No. US20030224374A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linaley, Peter
APPLICANT: Roberts, Chris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 005727
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1191
PRIOR FILING DATE: 2002-03-05
                                                                                       TYPE: DNA
CORGANISM: Homo sapiens
US-10-205-823-424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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   PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001/09/26
PRIOR FILING DATE: 2001/09/26
PRIOR FILING DATE: 2001-09-10
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SEQ ID NO 323
LENGTH: 1154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 284; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-323
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Best Local Similarity
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Publication No. US20040175744A1
GENERAL INFORMATION:
APPLICANT: METGEON LEG
TITLE OF INVENTION: POLYNUCLECTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
TITLE OF INVENTION: IN CERTAIN CANCERS
TITLE OF INVENTION: IN CERTAIN CANCERS
FILE REFERENCE: Mergen - 0010B
CURRENT PELING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: US 60/447,900
PRIOR PILING DATE: 2003-02-13
NUMBER OF SEQ ID NOS: 385
SOFTWARE: Patentin version 3.2
SEQ ID NO 136
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TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION UNMERR: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/225,149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 CAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGCCACTGTCGTCCAGTGCCATGCAGT 157
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Pred. No. 6.3e-80;
0; Mismatches 2; Indels 0;
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Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Sebastian HOERSCH
APPLICANT: Sebastian HOERSCH
APPLICANT: Stubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISEY
APPLICANT: Michael MORRISEY
APPLICANT: AMI SEN
APPLICANT: AMI SEN
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Gordon B. MILLS
Robert C. BAST, Jr.
Resemarie SCHMANDT
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Best Local Similarity 99.3%;
Matches 284; Conservative
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; ORGANISM: Homo sapiens
US-10-775-920-136
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Karen GLATT
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US-10-097-340-323
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APPLICANT: G19Nne, KICHET A.

APPLICANT: Hevezi, Peter A.

APPLICANT: Hevezi, Peter A.

APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: Mateon, Susan R.

APPLICANT: Wateon, Susan R.

APPLICANT: Wateon, Susan R.

TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Diagnosis of Cancer, CURENT Boss Biotechnology, Inc.

TITLE REFERENCE: 018501-012500US

TITLE OF INVENTION: Methods of Screening for Modulators of Cancer, TITLE OF INVENTION: Methods of Screening for Modulators of Cancer, CURRENT APPLICATION NUMBER: US 09/663,733

PRIOR FILING DATE: 2000-09-15

PRIOR PELICATION NUMBER: US 60/335,94

PRIOR FILING DATE: 201-11-12

PRIOR PELICATION NUMBER: US 60/332,464

PRIOR FILING DATE: 2001-11-21

PRIOR FILING DATE: 2001-11-21

PRIOR FILING DATE: 2001-11-21

PRIOR APPLICATION NUMBER: US 60/340,376

PRIOR APPLICATION NUMBER: US 60/347,211

PRIOR APPLICATION NUMBER: US 60/347,211

PRIOR APPLICATION NUMBER: US 60/347,349

PRIOR PILING DATE: 2002-01-08

PRIOR PILING DATE: 2002-01-10

PRIOR PILING DATE: 2002-01-10
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Pred. No. 6.4e-80;
0; Mismatches 2; I
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: PREUSEQ for Windows Version 4.0
SEQ ID NO 422
LENGTH: 1154
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Publication No. US20030232350A1
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Best Local Similarity 99.3%;
Matches 284; Conservative (
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APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-422
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PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 603
LENGTH: 1278
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95.2%; Score 282.8; DB 17; Length
Best Local Similarity 99.3%; Pred. No. 6.6e-80;
Matches 284; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-10-295-027-603
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Search completed: August 27, 2005, 11:33:34 Job time : 546.032 secs THIS PAGE BLANK (USPTO)

nucleic

Run on:

Seguence:

Title: Perfect

Searched:

Database

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PAT 22-JAN-2000
AX978173 Sequence
BD11032 EST and e
Continuation (5 of
AC117914 Rattus no
E30506 Gene RecQ5
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CQ7831098 Sequence
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CQ873927 Sequence
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AC106606 Rattus no
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Nees, M. and Duerst, M.
Nees, M. and Duerst, M.
Parent: WO 9423775-A 2 04-UUN-1998;
DEUTSCHES KREBSFORSCH (DE); NEES MATTHIAS (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ACTITICGAGIGCCAGAACCCAAGGAGGIGCAAAIGGACAGAGCCAIACIGCGIITAIAGCG
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Pred. No. 1.6e-71;
0; Mismatches 3; Indels
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/db_xref="taxon:32644"
               BD113032
LMFLCHR16_04
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Matches 258
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AUTHORS
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JOURNAL
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                                                                                                            August 27, 2005, 07:03:53 ; Search time 1386.39 Seconds
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                              - nucleic search, using sw model
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AK092545
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AC083841
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BC049723
AC119786
AC120775
AC151012
AR417479
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Maximum DB seq length: 200000000
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93.7 1028
48.1 2724
47.7 100079
47.7 151805
47.7 203375
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gb_ov:,
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GCCGTGAAAATATTTCCACGTTTTTTCATGGTTGCGAACAGGTGCTCCGCTGGTTGTGCCA 181 GCGATGGAGACCCAAGCCAGAGAGAGAGCGGTTTCTCCTGGAAGAGCCCATGCCTTC

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181

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AC119786 Rattus no AC120775 Rattus no AC151012 Callithri AR417479 Sequence

14.3 113.9 113.9 113.9

Result

GCGATGGAGAGCCCAAGCCAGAGGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTC

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/profein id="Cab69339.1"
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/db_xref="G1:6733554"
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LLEEEPMPFFYLKCCKIRYCNLEGPPINSSVFKEYAGSMGESCGGLWLAILLLASIAA
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                                                     Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
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/db_xref="taxon:32644"
/db_xref="taxon:32644"
/note="unnamed protein product; Protein sequence is conflict with the conceptual translation"
                                                                                                                                                                                                                                                                                        tch

34.9%; Score 247.8; DB 6; Length 421;
al Similarity 97.3%; Pred. No. 8.3e-69;
252; Conservative 0; Mismatches 7; Indels 0.
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Patent: WO 02068579-A 14147 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
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Machl, A. and Kubbies, M.
FANCONI-GEN II
PATCH: WO 9845428-A 1 15-OCT-1998;
MACHL ANDREAS (DE); KUBBIES MANFRED
LOCATION/Qualifiers

    .421
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/db_xref="taxon:9606"

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Sequence 1 from Patent WO9845428.
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                                       REFERENCE
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DNA for evaluating progress potential of cervical diseases.
BD023237
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27-NOV-1996 DE 19649207.8
MATHAR DIRUST, MATHAR NES.
CI2N15/09,CO7K14/00,CO7K16/00,C12P21/02,C12Q1/68,C12Q1/70, PC
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1 (bases 1 to 261)

Burust, M. and Ness, M.

DNA for evaluating progress potential of cervical diseases

Patent: JP 2001504703-A 2 10-APR-2001;

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PD 10-APR-2001
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Pred. No. 1.6e-71;
0; Mismatches 3; Indels
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    ..261
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                      TTTTACCTCAAGTGTTGTAAA 261
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JP 2001504703-A/2.
Homo sapiens (human)
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al Similarity 98.9%;
258; Conservative (
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Homo sapiens
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PD 10-APR-
PR 12-NOV-
PR 27-NOV-
PI MATHIAS
PC C12N15/
PC C12N15/
CC Strande
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FH Key
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Klausher, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altechul, S.F., Zeeberg, B., Buetcow, K.H., Schaefer, C.F., Bhat, N. K.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Schoetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bossak, S.A., McEwan, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Wazny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Boutfard, G.G., Blakesley, R.W., Touchman, J. W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Alb Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens cDNA for differentially expressed CO16 gene, mRNA (CDNA clone IMAGE:3457263), partial cds.
BC001291.1 GI:12654892
                                                                                               /translation="Mallalluvvalprvwtdanxtarordprdsortdegdnrvwch
vcerentfeconfreckwtepvcviaavkifprffwakcggaggagardferrf
Lleepwpffylkcckifrycnlegppinssvfkeyagsmgescgglwlaillillasiaa
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1373)
/note="unnamed protein product; Protein sequence is in conflict with the conceptual translation"
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Matches 252; Conservative
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arzayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.ehgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Series: IRAK Plate: 4 Row: 1 Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 24308142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="CapradppwaplgTmallalllvValprvwTdanltrarQrdped
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                                                Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 TTTCGAGTGCCAGAACCCAAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 94.9%; Score 247.8; DB 9; Length Best Local Similarity 97.3%; Pred. No. 8.6e-69; Matches 252; Conservative 0; Mismatches 7; Indels
Direct Submission
Submitted (11-DEC-2000) National Institutes
                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="synonym: HSJ001348"
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|db_xref="LocusID:54742"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:3457263"
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LLEEPMPFFYLKCCKIRYCNLGGANLSTHQCSKNMLGAWVRAVVGCGWPPLQ
                                    HSJ001348 10-FEB-1999 HOMO sapiens CDNA for differentially expressed CO16 gene.
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Machia.W., Planitzer,S.A., Rueckels,M. and Kubbies,M.
Identification and characterization of a novel cDNA not expressed in Fanconi anemia fibroblasts and B-cell lines
                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (12-58E-1997) Machl A.W., TR-BY1, Boehringer Mannheim
GmbH, Nonnenwald 2, 82377 Penzberg, GERMANY
Location/Qualifiers
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                                                                                     AJ001348.1 GI:2407910
CO16 gene.
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256. .>927
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Cta,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sakamatsu,A., Hayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishin,S., Yamamotco,J. Saito,K., Kawai,Y., Isono,Y., Nakamura,Y. Ishin,S., Yamamotco,J., Saito,K., Yawai,Y., Isono,Y., Nakamura,Y., Sudo,H., Minomi,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Mainomi,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Nainomi,Ya,K., Ishibashi,T., Yamashi,T., Xamai,T., Yamashi,T., Yamashi,T., Yamashi,T., Sasaki,T., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Shiohata,N., Shingta,K., Makebe,H., Hishigaki,H., Matanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Ramashi,T., Xamashi,T., Xomana,M., Yashigama,M., Jashigeta,K., Rawakami,T., Maranabe,M., Komatsu,Y., Mizushima-Sugano,J., Satoh,T., Shitota,Y., Matanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shitota,Y., Matanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shitota,Y., Matanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shitota,Y., Makamura,M., Komatsu,Y., Nakashima,Y., Nakashi,Y., Yamashita,R., Nakashi,Y., Yamashi,Y., Yamashi,Y., Nakashi,Y., Yamashi,Y., Nakashi,Y., Nakashi,Y., Yamashi,Y., Nakashi,Y., Yamashi,Y., Nakashi,Y., Yamashi,Y., Nakashi,Y., Yamashi,Y., Yamashi,Y., Yamashi,Y., Yamashi,Y., Yamashi,Y., Yamashi,Y., Yamashi,Y., Yamashi,Y., Yamashi,Y., Yamas
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                                                                                         PRI 30-JAN-2004
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Kodaira, H., Furnya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K.,
Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M.,
Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S.,
Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T.,
Kimura, K., Xamashita, H., Marsuo, K., Nakamura, Y., Sekine, M.,
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Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
NEDO human cDNA sequencing project
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                       Homo sapiens cDNA FLJ35226 fis, clone PROST2001138, moderately similar to Homo sapiens cDNA for differentially expressed CO16
                                                                                         linear
                                                                                                                                                                                                                                                                                     AK092545.1 GI:21751165
oligo capping; fis (full insert sequence)
Homo sapiens (human)
                                                                                         mRNA
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                                                                                         2724 bp
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FEATURES

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Direct Submission

Direct Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

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All repeats were identified using RepeatMasker:

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

Ruttp://ftp.genome.washington.edu/RM/RepeatMasker:html

Ruttp://ftp.genome.washington.edu/RM/RepeatMasker:html
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreitza, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., McCarthy, M., McKernan, K., Malthews, C., McCarthy, M., McBwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Reta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schuer, S., Schupback, R., Seman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Wille, R., W., W., Wann, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Subnission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
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/clone_lib="CITD1 Human BAC"
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/organism="Homo sapiens"
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/rpt_family="GA-rich"
553. .1074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 TITCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CCAGCGAACGGACGAGGTGACAATAGAGTGTGGTGTCATGCTTGTGAGAGAAAACAC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100079)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC108002 100079 bp DNA linear PRI 07-MAR-20
Homo sapiens chromosome 8, clone CTD-2292P10, complete sequence.
AC108002
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                                                                                                                                                                                                                                                                                                                           48.1%; Score 125.6; DB 9; Length 2724; 85.4%; Pred. No. 3.1e-29; ive 0; Mismatches 24; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 cérchagranterreserreses 269 cérchage de 269 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone CTD-2292P10
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                                                                                                                                                      /clone="PROST2001138"
         Location/Qualifiers
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Matches 140; Conservative
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/rpt_family="AluJo"
complement(17030. 17447)
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/rpt family="AT rich"

complement (14787. .15222)

/rpt family="LIMEc"

complement (15239. .15395)

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complement(16766, .1702^\/rpt_family
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complement(11625, .11841)
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complement (16565. .16761)
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complement (6991. 7358)
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7694. 7789
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5015. .5035
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075. .1372
                                                 rpt_family="BaEV-int"
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                                                                                                                                                                                                                     family="GC_rich"
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                 rpt_family="Aluy"
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4036. .14299
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A RY235094.3 GI:14280185

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_CANCELLED.
Homo sapiens (human)
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF235094 105156 bp DNA linear HTG 26-JUL-2002
Homo sapiens chromosome 8 clone CTA-391H8 map 8q24, WORKING DRAFT
SEQUENCE, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 AGAGACCCAAGCCAGAGGAGAAGCGGTTCTCCTGGAAGAGCCCATGCCCTTCTTTTACC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29028 AAATATTICCACGTTTTTTCATGGTTGCGAAGCAGTGCTCCGCTGGTTGTGCAGCGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 AAATATTTCCACGTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGCGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 100079;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 124.4; DB 9;
Pred. No. 8.5e-29;
0; Mismatches 6
complement (17495. .17715)
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complement (17904. .18230)
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/rpt family="MLT1A2"
/rpt family="LiMEC"
/rpt family="LiMEC"
complement (18789. .18950)
/rpt family="LiMEC"
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Best Local Similarity 95.5%;
Matches 128; Conservative
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McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, T., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (17-0cT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 6, 2000 this Sequence version replaced gi:7341925.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center first mane: 150 18

Sequencing vector: Mai M7815; 41% of reads
Sequencing vector: Plasmid; n/a; 59% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.560731
Consensus quality: 151299 bases at least Q40
Consensus quality: 151299 bases at least Q40
Consensus quality: 152267 bases at least Q20
Insert size: 133000; sum-of-contigs
Quality coverage: 10.5 in Q20 bases; agarose-fp

**NOTE: This is a "working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
** is not known and their order in this sequence record is
** runs of N, but the exact sizes of the gaps are unknown.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will
** be preserved.
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73 59832: gap of 100 bp
833 62883: contig of 3051 bp in length
884 62883: gap of 100 bp
984 67564: contig of 4581 bp in length
565 67664: gap of 100 bp
665 121673: contig of 54009 bp in length
674 121773: gap of 100 bp
774 153005: contig of 31232 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence submissions@genome.wi.mit.edu
Center project name: L3500
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/db_xref="taxon:9606"
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vector side:left"
5983. .62883
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62984. .67564
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121774. .153005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92512 AAATATTTCCACGTTTTTTCATGGTTGCGAAGCAGTGCTCCGCTGGTTGTGCAGCGATGG 92453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birran, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Bouslavkiy, L., Boukhgalter, B., Boowin, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Klein, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 AGAGACCCAAGCCAGAGGAAAGCGGTTTCTCCTGGAAGAGCCCCATGCCCTTCTTTACC 247
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo.sapiens, clone RP11-15018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                         ### 13020: contig of 30320 bp in length 321 30420: gap of unknown length 421 59704: contig of 29284 bp in length 420 59804: gap of unknown length 1005 83308: contig of 29284 bp in length 1009 83408: gap of unknown length 1009 95522: contig of 12114 bp in length 1523 95622: gap of unknown length 1568 9667: contig of 2945 bp in length 1568 9667: contig of 2945 bp in length 1568 101380: contig of 2913 bp in length 10180: contig of 2713 bp in length 103751: contig of 2713 bp in length 103751: contig of 2713 bp in length 1681 103751: contig of 2713 bp in length 1682 105156: contig of 1305 bp in length 16852 105156: contig of 1305 bp in length 16852 105156: contig of 1305 bp in length 16852 105156: contig of 1305 bp in length.
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Pred. No. 8.6e-29;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .105156
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ACO11976.5 GI:11560232
HTG: HTGS PHASE1; HTGS_DRAFT.
HOMO SADIENB (human)
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Best Local Similarity 95.5%;
Matches 128; Conservative
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Ulreck submission

Ulreck submission

Besearch, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

123 (bases 1 to 157839)

Birren, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,

Andergon, S., Barna, N., Bastlan, V., Boguslavkiy, L., Boukhgalter, B.,

Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,

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Retta, R., Rieback, M., Kalley, R., Rise, C., Rogov, P., Roman, J.,

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Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                   128 AAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGCGATGG 187
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo appiens chromosome, clone RP11-119A16
                                                                Gaps
        DB 2; Length 153005;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACU15/18 157839 bp DNA linear
Homo sapiens clone RP11-119A16, 4 unordered pieces.
AC015718
                                                           Indels
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_CANCELLED.
HOmo sapiens (human)
     Score 124.4; DB 2;
Pred. No. 8.6e-29;
0; Mismatches 6;
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                                95.5%;
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Query Match
Best Local Similarity 95.5
Matches 128; Conservative
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203375 bp DNA linear PRI 25-WAY-2002 Homo sapiens chromosome 8, clone RPI1-706C16, complete sequence. AC083841.9 GI:21206312
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 8, clone RP11-706C16
Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 9, 2002 this sequence version replaced gi:14029953. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                  ....---- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. On the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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1974 8073: gap of 100 bp
1074 81857: contig of 73784 bp in length
1858 81957: gap of 100 bp
1858 136278: contig of 54321 bp in length
1279 136379: gap of 100 bp
1379 157839: contig of 21461 bp in length.
Location/Qualifiers
                                                                                                                                                                                                         /clone="RP11-119A16"
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Best Local Similarity 95.5
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Submitted (13-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Establishment of the control of th
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Direct Submission
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AUTHORS
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TITLE

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Submitted (25-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 25, 2002 this sequence version replaced gi:20303671. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
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/rpt_family="AluY"
3858. .4201
                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="L1MA8"
1420. .2469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              )80. - . 1040
/rpt_family="THE1C"
1041 - . 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'rpt_family="L1MA8"
complement(1591. .2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121. .3546
rpt_family="L1MA8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_family="L1MA2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34. ... 978
rpt_family="THE1C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt_family="L1MA3"
094. .1586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1820. .3120
rpt_family="AluSg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="L1MA8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432. . . 625
/rpt_family="MSTA"
526. . . 733
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Base-by-base quality values are not generally visible from the
GenBank flat file format but are available as part
of this entry's ASN.1 file.
Siddiqui,R., Taudien,S., Wen,G., Schlegelberger,B., Siebert,R.,
Rosenthal,A. and Platzer,M.
Chromosome 8 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pleces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing the sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1000 54681: contig of 11682 bp in length 4882 54781: gap of unknown length 6782 60929: contig of 6148 bp in length 6782 61939: contig of 6148 bp in length 1030 79991: contig of 18962 bp in length 6992 80091: gap of unknown length 6092 103247: contig of 23156 bp in length. Location/Qualifiers 1.103247
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contig of 4364 bp in length
contig of 4364 bp in length
contig of 4217 bp in length
gap of unknown length
contig of 3243 bp in length
contig of 7674 bp in length
contig of 7674 bp in length
contig of 5690 bp in length
gap of unknown length
contig of 5690 bp in length
gap of unknown length
contig of 5890 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1510: contig of 1510 bp in length
1610: gap of unknown length
4022: contig of 2412 bp in length
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8486:
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12803:
12903:
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33268:
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54682
54782
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297111
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                                                                                                                                                                                                                                                                                                                                                             COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184679 AGAGACCCAAGCCAGAGGGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTCTTTTACC 184620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF176678 103247 bp DNA linear HTG 26-JUL-2002 SEQUENCE, 13 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187
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Mammalia; Butheria, Primates; Catarrhini, Hominidae, Homo.
1 (bases 1 to 103247)
Schilhabel, M. B., Baumatt, C., Blechschmidt, K., Dette, M., Jahn, N.,
Lehmann, R., Menzel, U., Polley, A., Reichwald, K., Schudy, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 AAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGCGATGG
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_CANCELLED.
Homo sapiens (human)
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/rpt_family="LiPB3"
complement[25625. .25798]
/rpt_family="Li"
25826. .27177
                                                                                                   complement (15107. 16745)
/rpt_family="MLT1A1-int"
complement (16775. 17008)
/rpt_family="MLT1A1"
17407. 19132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="MSTA"
0142..20401
                                 complement (14739. .15100) /rpt_family="MLT1A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="MLT2C1"
20520. .20882
/rpt_family="THE1C"
20925. .21058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="MLT2C1"
complement(19728..20
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0402. .20436
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2032. .22331
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0437. .20514
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22570. .25000
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           family="(TG)n"
                                                                                                                                                                                                                                                      7407. .19132
rpt_family="ERVL"
9133. .19543
                                                                                                                                                                                                                                                                                                                                                                                          rpt_family="ERVL"
9663..19727
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1940. .22004
                                                                                                                                                                                                                                                                                                                                                         rpt_family="MSTC"
9544. .19657
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/rpt_family="L1"
21060. .21440
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:510<u>5</u>.
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Maus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Butcow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Staplecon, M., Soares, M.M. B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T. B., Toshiyuki, S.

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malle, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Fahey, J., Helton, E., Retteman, M., Madan, A., Rodrigues, S.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Boufeard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Butcerfield, Y.S., Krzywinski, M.I., Shaiska, U., Smailus, D.E.,

Butcerfield, Y.S., Krzywinski, M.I., Salska, U., Smailus, D.E.,

Chomeroh, A., Socien, J.B., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

Broce, Natl. Acad. Sci. U.S. W. 99 (26), 16899-16903 (2002)
                                                                                                           643 bp mRNA linear ROD 07-OCT-2003
Mus musculus RIKEN cDNA 2410015A16 gene, mRNA (cDNA clone MGC:58713
IMAGE:6743692), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.AG.B. Consortium/Linn at: http://image.llnl.gov Series: IRAL Plate: 46 Row: d Column: 24. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (11-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jonathan Kuo, NIMH
CDNA Library Preparation: Michael Brownstein / Ted Usdin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca
  155 TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
                                                                                                                                                                                                                                                       BC049723.1 GI:29437322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 643)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg, R.
                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory
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                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                   ORGANISM
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PUBMED
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TITLE
JOURNAL
                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                 RESULT 15
BC049723
                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                   19301 AGAGCCCAAGCCAGAGGAGATGCGGTTTCTTTGGAAGAGCCCCATGCCCTTCTTTACC 19360
                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BV203566 201 bp DNA linear STS 10-JUN-2004 sqnm212498 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            188 AGAGACCAAAGCCAGAGGGGTTTCTCCTGGAAGACCCATGCCCTTCTTTACC 247
                                                                                                                                                                                                                                                                                                                                   128 AAATATTICCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGCGATGG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (basea I to 201)
Nelson, R.M., Marnellos, G., Kammerer, S., Hoyal, C.R., Shi, M.M., Cantor, C.R. and Braun, A.
Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
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                                                                                                                                                                                                                          Length 103247;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequenom, Inc.
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                                       46.4%; Score 121.2; DB 2; 94.0%; Pred. No. 9.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .201
/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/clone lib="Human DNA (Sequenom)"
<1. .>201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

40.2%; Score 105; DB 11;
Best Local Similarity 98.1%; Pred. No. 1.4e-22;
Matches 105; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 201.
                                                                                                                                                                                                                                                                              0; Mismatches
organism="Homo sapiens"
                       /mol_type="genomic_DNz"/db_xref="taxon:9606"
/chromosome="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                        /map="8q24.3"
/clone="CTA-93D7"
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BV203566.1 GI:48172981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 TCAAGTGTTGTAAA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                         Matches 126; Conservative
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KEYWORDS
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| J. -648
| J. -64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 GAAAAGAAATTCTGTTGTTGGCGTCACACAATTTTTGAACGTTTCTTCTATGTGTCG 243
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14.3%; Score 37.2; DB 10; Length 643;
Best Local Similarity 53.4%; Pred. No. 1.2;
Matches 78; Conservative 0; Mismatches 68; Indels 0.
/clone="MGC:58713 IMAGE:6743692"
/tissue type="Testis, mouse"
/clone_lib="NIH MGC_169"
/lab host="DH10B"
/note="Vector: pDNR-LIB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 AAACAGTGCACCCGAAGGTGTCCAAC 269
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Search completed: August 27, 2005, 09:49:26 Job time : 1389.39 secs

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/lab_host="DHIOB"
/clone lib="NCI_CGAP_Lu24"
/clone lib="NCI_CGAP_Lu24"
/note="Corgan: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento
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AI583197 tq64g09.x
AI703260 wd8a2b10.x
BE551234 7b56d09.x
AI828018 wf12f09.x
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(without alignments)
4080.665 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries

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clone lib="NCI CGAP Lu24"
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/tissue_type="carcinoid"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    503 TTACCTCAAGTGTTGTAAA 521
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                                                                                                                                                          Query Match
Best Local Similarity 97.3%;
Matches 252; Conservative
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AUTHORS
TITLE
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Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-blo.llnl.gov/bbrp/image/image.html

Seq primer: -40UP from Gibco

High quality sequence stop: 463.
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/lab_host="DH10B (phage-resistant)"
/clone lib="NCI_CGAP_Lu19"
/note="Organ: lu10" Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AISB3197 560 bp mRNA linear EST 06-APR-1999 tq64g09.xl NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2213632 3'
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                                                                                                                                           62
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1 (bases 1 to 560)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:2213632"
/tissue type="squamous cell carcinoma, poorly
differentiated (4 pooled tumors, including primary and
metastation.
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                                                                                                  Gaps
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                                                       Length 559;
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                                                       Query Match 94.9%; Score 247.8; DB 2; Best Local Similarity 97.3%; Pred. No. 1.9e-68; Matches 252; Conservative 0; Mismatches 7;
Soares and M. Fatima Bonaldo.
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/db xref="taxon:9606"
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Unpublished (1997)
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AI583197
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AI703260 560 bp mRNA linear EST 17-DEC-1999 wd82b10.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2338075 3' similar to TR:015227 015227 CDNA FOR DIFFERENTIALLY EXPRESSED CO16
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- oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M Patima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                 443 GATGGAGAGACCCAAGCCAGAGGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCCTTCTT
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                                                                                                                                                                                                                                         Gaps
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0
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Pred. No. 1.9e-68;
0; Mismatches 7; Indels 0
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ORIGIN

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/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lus was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1417991 and 1520904-1523439). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmer-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NGT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@lange.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: S07.
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1 (Dases 1 to 575)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
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0
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/clone="IMAGE:3232241"
/tissue_type="carcinoid"

    .575
    /organism="Homo sapiens"

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BE551234
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/lab_host="DH10B"
/clone lib="NCI_CGAP_Lu24"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs
1414920-1417991 and 1520904-1522439). Subtraction by Bento
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/clone lib="Soares NFL T GBC_S1"
/note="Organ: pooled; Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 845 Std Error: 0.00
Seq primer: 940UP from Gibco
High quality sequence stop: 467.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 464 GATGGAGAGACCCAGAGGGGGAAGAGCGGTTTCTCCTGGAAGAGCCCATGCTTCTT
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                                                                                                                                                                                                                                                                                                DB 2; Length 575;
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                              tch 94.9%; Score 247.8; DB 2; al Similarity 97.3%; Pred. No. 1.9e-68; 252; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                               Soares and M. Fatima Bonaldo.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2350409"
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AI828018.1 GI:5448610
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Best Local &
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Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed, and ss circles were made in vitro. F01lowing HAP purification, this DNA was used as tracer in subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729966-731399, Subtraction by Bento Soares and M. Patima Bonaldo. "
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTP/DTP

CDNA.ibrary Preparation: Ling Hong/Rubin Laboratory

CDNA.ibrary Prayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Inforte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://inage.lln.gov

Right quality sequence start: 29

High quality sequence start: 29

High quality sequence stor: 640.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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60253526771 NIH_MGC_41 Homo sapiens CDNA clone IMAGE:4654072 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_hogt="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                                                                Length 619;
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/db_xref="taxon:9606"
/clone="IMAGE:4654072"
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/clone lib="NIH MGC_41"
/note="Organ: skin; Vector: pOTB7; Site l: XhoI; Site 2:
EcoR1; cDNB made by Oligo-dT priming. Directionally cloned
into EcoR1/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Babersely) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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602294533F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4389033 5',
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium(LLNL)

Round through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMM10076 row: b column: 10

High quality sequence stop: 608.

High quality sequence stop: 608.
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1. (Dases 1 to 647)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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/note="Torgan: bone; Vector: pCMV-SPORT6; Site_1: Not1;
                                                                                                                                                                                                                                                                                                                                                                332 CGTGAAATATTTTCCACGTTTTTTTCATGGTTGCCGAAGCAGTGCTCCGCTGGTTGTGCAGCAGC
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_86"
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                                                                                                                                                                                                                                              94.9%; Score 247.8; DB 97.3%; Pred. No. 2e-68; ive 0; Mismatches
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/db_xref="taxon:9606"
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BG027935.1 GI:12417029
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//db xref="hRNA"
/db xref="hRNA"
/db xref="hRNA"
/clone="lnAGS15481773"
/tlab_host="hH0B (phage-resistant)"
/clone=lib="hNH MGC_41"
/clone=lib="hNH MGC_41"
/note="forgan: skin: Vector: porB7; site 1: xho1; site 2:
RcoR1; cDNA made by oligo-dr priming. Directionally cloned
into EcoR1/kho1 sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
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AGENCOURT G701603 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5481773
5', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rub
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information clone distribution: MGC clone distribution information clone found through the I.M.G.E. Consortium/Link at:
http://image.lln.gov
Plate: Lick2006 row: m column: 06
High quality sequence stop: 680.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 679)
                                 Average insert size 1.533 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                           Score 247.8; DB 4; Length
Pred. No. 2e-68;
0; Mismatches 7; Indels
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Best Local Similarity 97.3%;
Matches 252; Conservative (
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/tissue_type="melanotic melanoma, cell line"
/lab host="billob (phage-resistant)"
/lobe lib="NIH MGC_112"
/lobe lib="NIH MGC_112"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following S' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Supersoript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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AGENCOURT 8507940 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6294463
E), mRNA sequence.
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NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2499 row: c column: 08
High quality sequence stop: 637.
                                                                                                                                                                                                                                                                                                                                                                                             225 TITCGAGTGCCAGAACCCAAGGAGGGGGAAATGGACAGAGCCATACTGCGTTATAGCGGC
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Superscript II RT (Life Technologies), Note: this NIH_MGC Library."
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                                                                                                                        Length 679;
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                                                                                                                           5.
                                                                                                                        94.9%; Score 247.8; DB 97.3%; Pred. No. 2e-68; ive 0; Mismatches
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/clone="IMAGE:6294463"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 684)

I 1 (bases 1 to 684)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: NIMH/LOG

CDNA Library Preparation: NIMH/LOG

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCWASSEs row: e column: 11

High quality sequence stop: 648.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BU500474 684 bp mRNA linear EST 12-SEP-2002
AGENCOURT 7860877 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:6103426
5', mRNA sequence.
BU500474
                                                                                                                                                                                                                                           217 TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC 276
                                                                                                                                                                                                                                                                                                                                                                                                                 337 GATGGAGACCCAAGCCAGAGAGAGAGGGGTTTCTCCTGGAAGAGCCCATGCCTTTTT 396
                                                                                                                                                                                                                                                                                                                                         277 CGTGAAAATATTTCCACGTTTTTTCATGGTTGCGAAGCAGTGCTCCGCTGGTTGTGCAGC 336
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                                                                                                                                                  157 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGGTGTTCATGTTTGTGAGAGAAAACAC
                                                                                                                                                                                                                                                                                             CGTGAAAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC
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                                                                                                     TITCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
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Score 247.8; DB 5; Length 682; Pred. No. 2e-68; 0; Mismatches 7; Indels 0
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  otch 94.9%; sal Similarity 97.3%; 252; Conservative
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Homo sapiens
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/db_xref="taxon:9606"
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EcoR1; cDNA made by oligo-dT priming. Directionally cloned
into EcoR1/Xhol sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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B 1 (bases 1 to 682)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate! LLCM2331 row: j column: 06

High quality sequence stopp: 660.
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AGENCOURT 8032883 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6091109
Forman Sequence.
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BQ679186.1 GI:21791865
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                                                      Query Match
                                                                               Local
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ilarity 97.3%; Pred. No. 2.8e-68;
Conservative 0; Mismatches 7;
                                 DB 5;
                              Score 247.8; DB 5
Pred. No. 2.2e-68;
                                                                                   0; Mismatches
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CRS90427.1 GI:50471234
HTC; CNSLT_CDNA.
HOMO SADIENS (human)
HOMO SADIENS
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                           94.9%;
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                                                       Best Local Similarity 97.3 Matches 252; Conservative
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/clone_lib="NAH MCC[126"
/clone_lib="NAH MCC[126"
/clone_lib="NAH MCC[126"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          909 bp mRNA linear EST 07-MAY-2002
AGENCOURT_6770142 NIH_MGC_126 Homo sapiens cDNA clone IMAGE:5810055
S', mRNA sequence.
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                                                                             204 TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGGGGC 263
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                                                                                                                                                                                                                                                              183 GATGGAGACCCAAGCCAGAGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT 242
                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: egapbe-rémail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium
CLONE distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2056 row: k column: 16
High quality sequence stop: 505.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 909)

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National Institutes of Health, Mammalian Gene Collection (MGC)
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Direct Submission
Submitted (20-JUJ-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. ö CR590427 2326 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CSODK010YP02 of HeLa cells Cot 25-normalized ö 122 182 302 182 242 242 303 GATGGAGAGCCCAAGCCAGAGGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT 362 224 62 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. Li, W. B., Gruber, C., Jessee, J. and Polayes, D. Pull-length cDNA libraries and normalization TTTCGAGTGCCAGAACCCAAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC 183 TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC CGTGAAAATATTTCCACGTTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC 243 GGTGAAATATTTCCACGTTTTTTCATGGTTGCGAAGCAGTGCTCCGCTGGTTGTGCAGC GATGGAGAGCCCAAGCCAGAGGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT Gaps Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Gaps ö ö Length 2326; /organism="Homo sapiens"
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```
Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
    Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
    Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
    CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LiAMIITy & row: h column: 20
    High quality sequence stop: 636.
    Location/Qualifiers
    I. 636
                                                                                                                                                                                                                                                                                                                                                            BI560005 636 bp mRNA linear EST 05-SEP-2001 603253476F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:5295811 5',
63 TITCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC 122
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                           183 GATGGAGAGCCCAAGCCAGAGGGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT
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| /tissue_type="cervical carcinoma cell line"
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E. (Bases I to 626)

E. (Bases I to 626)

NH+MGC http://mgc.nci.nih.gov/.

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Sequencing by: Incyte Genomics, Inc.

CDNA Library Arrayed by: Incyte Genomics, Inc.

CDNA Ederibution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLAM8459 row: k column: 15

High quality sequence stop: 585.

Location/Qualifiers
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                          285 CGTGAAAATATTTCCACGTTTTTTCATGGTTGCGAAGCAGTGCTCCGCTGGTTGTGCACG
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llarity 96.9%; Pred. No. 6.4e-68;
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

* Query Match Length DB ID  Description	261 13 US-10-079-954-2 Sequence 2, Appli 672 17 US-10-295-027-339 Sequence 339, App 672 18 US-10-188-832-172 Sequence 172, App 754 17 US-10-172-118-2114 Sequence 2414, Ap 754 18 US-10-442-887-2414 Sequence 2414, Ap 754 18 US-10-442-887-2414 Sequence 2414, Ap 755 9 US-10-977-801-1	14 IIS-10-199-44B-1
* Query Match Le	1000.0 94.0 9.49.0 9.49.0	94.0
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US-10-295-027 US-10-264-049 US-10-723-860 US-10-238-443	US-10 US-10 US-10 US-10 US-10	17 US-10-443-108-1 17 US-10-188-646-4 19 US-10-807-897-28 19 US-10-807-897-26 14 US-10-235-026-1 20 US-10-839-882-37 14 US-10-244-586-1 17 US-10-188-646-11	4400000	US-10-027-632- US-10-027-632- US-09-989-723-1 US-09-989-723-1 US-09-989-727-1 US-09-989-727-1	9 US-09-989-732-19 0 US-09-991-073-19 9 US-09-990-442-19 9 US-09-991-63-19 9 US-09-993-604-19 9 US-09-990-456-19
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## ALIGNMENTS

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US-10-079-954-2

i Sequence 2, Application US/10079954

j Sequence 2, Application US/20020168661A1

j GENERAL INFORMATION:
    GENERAL INFORMATION:
    JAPLICANT: DURET, Matthias
    APPLICANT: DAM TON EXALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
    TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
    TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
    TRIOR APPLICATION NUMBER: US/10/079,954
    CURRENT FILING DATE: 1999-09-03
    PRIOR PILING DATE: 1999-09-03
    PRIOR PILING DATE: 1997-11-12
    PRIOR APPLICATION NUMBER: DE 196 49207
    PRIOR PILING DATE: 1997-11-27
    NUMBER OF SEQ ID NOS: 4
    SEQ ID NOS: 4
    CORGANISM: Homo sapiens
    US-10-079-954-2

    Query Match
    Guery Match
    Matches 261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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386 182 446 242 506

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APPLICANT: Application US/10188832

Sequence 172, Application US/10188832

Sequence 172, Application US/10188832

Sequence 172, Application US/10188832

Sequence 172, Application NO: US20040076955A1

APPLICANT: Mack, David H.

APPLICANT: Aziz, Natasha

APPLICANT: Eos Biotechnology, Inc.

TITLE OF INVENTION: And Methods of Diagnosis of Bladder Cancer, Compositions

TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder

TITLE OF INVENTION: Cancer

TITLE OF INVENTION: Cancer

FILE REFERENCE: 018501-002330US

CURRENT FILING DATE: 2002-11-22

PRIOR PILING DATE: 2001-00-03

PRIOR FILING DATE: 2001-00-03

PRIOR PELING DATE: 2001-00-03

PRIOR PELING DATE: 2001-11-08

PRIOR PELING DATE: 2001-11-08

PRIOR PELING DATE: 2001-11-08

PRIOR PELING DATE: 2001-11-13

PRIOR PELING DATE: 2001-11-08

PRIOR PELING DATE: 2001-11-03

PRIOR PELING DATE: 2001-11-03

PRIOR PELING DATE: 2001-11-03

PRIOR PELING DATE: 2001-11-03

PRIOR PELING DATE: 2001-11-13

PRIOR PELING DATE: 2001-11-03

PRIOR PELING DATE: 2001-04-12

PRIOR PELING DATE: 2001-04-12
387 CGTGAAAATTTTCCACGTTTTTTCATGGTTGCGAAGCAGTGCTCCGCTGGTTGTGGAGC
                                                                                                                                                                                                                            CGTGAAAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC
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US-10-188-832-172
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APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Mark, David H.
APPLICANT: Mark, David H.
APPLICANT: Mark, David H.
APPLICANT: Matson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
TITLE OF INVEXTION: Methods of Exceening for Modulators of Cancer
TITLE OF INVEXTION: Methods of Screening for Modulators of Cancer
TITLE OF INVEXTION: Methods of Screening for Modulators of Cancer
TITLE OF INVEXTION: Mumber: US 006-03-10-13
PRIOR PELLING DATE: 2000-10-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-24
PRIOR FILING DATE: 2001-11-24
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2001-12-14
PRIOR FILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-03
                                                                                                    61 ACTITICGAGIGCCAGAACCCAAGGAGGIGCAAAIGGACAGAGCCAIACTGCGIIAITAIAGCG
                                                                                                                                                                                                                               121 GCCGTGAAAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCCGCTGGTTGTGCA
                                                                                                                                                                                                                                                                                                                                                       61 ACTITICGAGIGCCAGAACCCAAGGAGGIGCAAAIGGACAGAGCCAIACIGCGITAIAGCG
                                                                                                                                                                                           GCCGTGAAAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCA
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94.9%; Score 247.8; DB 17; Length 672;
Best Local Similarity 97.3%; Pred. No. 8.5e-78;
Matches 252; Conservative 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
US-10-295-027-339
US-10-295-027-339
i Sequence 339, Application US/10295027
i Publication No. US20030232350A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTACCTCAAGTGTTGTAAA 261
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APPLICANT: A212, Nacasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/10/342,887
                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
CORGANISM: Homo sapiens
US-10-342-887-2414
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STRANDEDNESS: both
TOPOLOGY: linear
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LOCATION:
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; LOCATION:
US-09-977-801-1
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US-10-342-887-2414/c
; Sequence 2414, Application US/10342887
; Sequence 2414, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: How, Wao
; APPLICANT: Roberts Christopher J.
; APPLICANT: Nao, Mao
; APPLICANT: Wan 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVERTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
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94.9%; Score 247.8; DB 17; Length 754;
Best Local Similarity 97.3%; Pred. No. 8.9e-78;
Matches 252; Conservative 0; Mismatches 7; Indels 0;
                                                                                                                                                                                      Sequence 2414, Application US/10172118
Publication No. US20030224374A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linaley, Peter
APPLICANT: Roberts, Chris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DATABASE ACCESSION NUMBER: Contig49058
DATABASE ENTRY DATE: 2001-06-18
507 TTACCTCAAGTGTTGTAAA 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
PUBLICATION INFORMATION
                                                                                                                                                              US-10-172-118-2414/c
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94.9%; Score 247.8; DB 19
Best Local Similarity 97.3%; Pred. No. 8.9e-78;
Matches 252; Conservative 0; Mismatches 7
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,632
FILING DATE:
FILING DATE:
SEQUENCE CHARACTERISTICS:
LENGTH: 1026 base pairs
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR PILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2002-05-14
PRIOR PILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 2414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 TTACCTCAAGTGTTGTAAA 240
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APPLICANT: Glynne, Richard
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Wacks, David H.
APPLICANT: Watson, Susan R.
TITLE OF INVENTION: Methods of Diagnosis of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REPERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US 60/350,027
CURRENT FILING DATE: 2000-09-15
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-29
PRIOR PLICATION NUMBER: US 60/347,319
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-01-01
PRIOR FILING DATE: 2001-01-01
PRIOR FILING DATE: 2002-01-08
PRIOR PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-08
                                                                                             582 TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGGGGC
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o. US20030232350A1
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## Sequence 753, Ar.

## Sex Ar.

## SENERAL INFORMATION:

## APPLICANT: Afar, Daniel

## APPLICANT: Afar, Daniel

## APPLICANT: Afar, Natasha

"TANT: Ginsberg, Wendy M.

"TANT: Ginsberg, Wendy M.

"TANT: Ginsberg, Wendy M.

"TANT: Afar, Mark C.

"TANT: Afar, Kurt C.

"TANT: Afar, Mark C.

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US-10-295-027-753
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Best Local Simi:
Matches 252; (
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        Score 247.8; DB 9; Length 1026;
Pred. No. 1e-77;
0; Mismatches 7; Indels 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: I BM PC compatible
COMPUTER: Tale PC compatible
CORPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EF
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATE: 19-Jul-2002
PRIOR APPLICATION DATE: US/09/977,801
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: US/09/402,632
FILING DATE: CUNKNOWN>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10199448
Publication No. US20030022858A1
GENERAL INFORMATION:
APPLICANT: Boehringer Mannheim GmbH
TITLE OF INVENTION: Fanconi-gene II
NUMBER OP SEQUENCES: 2
NUMBER OF SEQUENCES: 2
STREET: Sandhofer Str. 112-132
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LOCATION: 430..924
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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             94.9%;
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LOCATION: 256..924
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COUNTRY: Germany
ZIPi 68305
Query Match
Best Local Similarity 97.31
Matches 252, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPOLOGY: linear
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US-10-199-448-1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-7232
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Best Local Similarity
Matches 63; Conserva
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                                                             CGTGAAAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC 182
                                                                             256 CGIGAAAATATTTCCACGTTTTTTCATGGTTGCGAAGCAGTGCTCCGCTGGTTGTGCAGG 315
                                                                                                                         GATGGAGACCCAAGCCAGAGAGAGAGTTTCTCCTGGAAGAGCCCATGCCCTTCTT 242
                                                                                                                                           316 GATGGAGAGACCCAAGCCAGAGGAGAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT 375
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Pred. No. 2.8e-77;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                         US-10-264-049-1723

Sequence 1723, Application US/10264049

Publication No. US20040005579A1

Publication No. US20040005579A1

SEMERAL INFORMATION:

APPLICANT: Birse et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAINS 1339

CURRENT APPLICATION NUMBER: US/10/264,049

CURRENT APPLICATION NUMBER: PCT/US01/18569

PRIOR APPLICATION NUMBER: PCT/US01/18569

PRIOR APPLICATION NUMBER: US 60/209,467

PRIOR PRILING DATE: 2001-06-07

NUMBER OF SEQ ID NOS: 4360

SOFTWARE: Patentin Ver. 3.1

LENGTH: 502
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Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: AZIZ, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
                                                                                                                                                                                  TTACCTCAAGTGTTGTAAA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.3%;
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Best Local Similarity 96.9
Matches 251; Conservative
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US-10-264-049-1723
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US-10-723-860-7232
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 63
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TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions of TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators FILE REFERENCE: 0582.0193.NDVS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR PLING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
LENGTH: 1745
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## Sequence 13, Application US/10238443

## Publication No. US20030083302A1

## CENERAL INFORMATION:

## APPLICANT: Donna T. Ward

## APPLICANT: Andrew T. Watt

## TITLE OF INVENTION: WITSENSE MODULATION OF RECQLS EXPRESSION

## PILE REPERENCE: RTS-0203

## CURRENT FILING DATE: US/09/798,185

## PRIOR PILING DATE: 2001-03-01

## NUMBER OF SEQ ID NOS: 92

## SEQ ID NO 13

## LENGTH: 417
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                                                                                                                                                                                                                                                                                                                                                                                                    89.5%; Score 233.6; DB 20; Length 96.2%; Pred. No. 1.5e-72; ive 0; Mismatches 9; Indels
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Matches 250; Conservative
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100 GGGATGGGAGTGGATAAAGCCAATGTCAGGTTTGTCGCCCATTGGAATATTGCCAAGTCT 159
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LOCATION: 580
OTHER INFORMATION: unknown
NAME/KEY: unsure
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LOCATION: 360
OTHER INFORMATION: unknown
                     OTHER INFORMATION: unknown
                                        FEATURE:
NAME/KEY: unsure
LOCATION: 478
OTHER INFORMATION: unknown
                                                                                                                                                                  LOCATION: 508
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                 LOCATION: 530
OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
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ORGANISM: Homo sapiens
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NAME/KEY: unsure
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NAME/KEY: unsure
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US-10-309-362-11
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US-10-238-443-11

Sequence 11, Application US/10238443

Sequence 11, Application US/10238443

Publication No. US20030083302A1

GENERAL INFORMATION:

APPLICANT: Donna T. Ward

APPLICANT: Andrew T. Watt

TITLE OF INVENTION: ANTISENSE MODULATION OF RECQLS EXPRESSION

FILE REPERENCE RTS-0203

CURRENT APPLICATION NUMBER: US/10/238,443

CURRENT FILING DATE: 2002-09-09

PRIOR FILING DATE: 2001-03-01

NUMBER OF SEQ ID NOS: 92

SEQ ID NO 11
      Sequence 10. 1. Application US/10309362

Publication No. US20030114412A1

GENERAL INFORMATION:

APPLICANT: Donna T. Wart

APPLICANT: Andrew T. Watt

ITLE OF INVENTION: ANTISENSE MODULATION OF RECQL5 EXPRESSION

FILE REFERENCE: RTS-0203

CURRENT APPLICATION NUMBER: US/10/309,362

CURRENT FILING DATE: 2002-12-03

PRIOR PILING DATE: 2001-03-01

NUMBER OF SEQ ID NOS: 92

SEQ ID NO 13

LENGTH: 417
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OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 360
OTHER INFORMATION: unknown
FEATURE:
NAME/KEY: unsure
LOCATION: 388
OTHER INFORMATION: unknown
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LOCATION: 440
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION:
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NAME/KEY: unsure
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US-10-309-362-13
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Sequence 10, Application US/10238443

Publication No. US20030083302A1

GENERAL INFORMATION:

APPLICANT: Donna T. Ward

APPLICANT: Andrew T. Watt

TITLE OF INVENTION: ANTISENSE MODULATION OF RECQLS EXPRESSION

FILE REPERBUCE RTS-0203

CURRENT APPLICATION NUMBER: US/10/238,443

CURRENT FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: US/09/798,185

PRIOR FILING DATE: 2001-03-01

NUMBER OF SEQ ID NOS: 92
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Pred. No. 0.14;
0; Mismatches 47; Indels 0
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Best Local Similarity 57.3%;
Matches 63; Conservative
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OTHER INFORMATION: unknown
NAME/KEX: unsure
LOCATION: 595
OTHER INFORMATION: unknown
OTHER INFORMATION:
             LOCATION: 388
OTHER INFORMATION: unknown
                                                                                                       OTHER INFORMATION: unknown FEATURE:
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NAME/KEY: unsure
LOCATION: 478
OTHER INFORMATION: unknown
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NAME/KEY: unsure
LOCATION: 538
OTHER INFORMATION: unknown
FEATURE:
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LOCATION: 557
OTHER INFORMATION: unknown
                                                                                                                                                                                                                                            LOCATION: 465
OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
                                                                                                                                                                                 OTHER INFORMATION:
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OTHER INFORMATION:
AME/KEY: ungure
                                                    FEATURE:
NAME/KEY: unsure
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NAME/KEY: unBure
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NAME/KEY: unsure
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; SEQ ID NO 10; TYPE: DNA ; TAPE: DNA ; ORGANISM: Home sapiens ; EATURE: US-10-238-443-10

Query Match

Query Match

Best Local Similarity 57.3%; Pred: No. 0.21;

Matches 63; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 84 GAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGCCGTGAAAATATTTCCAGTTT 143

Qy 144 TTTCATGGTTACAGGTTCTCGCTGTTGCAGCGATGCAAGATATTGCCAAGTT 1144

Qy 144 TTTCATGGTTACACAGGAGTCTGGTGGTGCGCGATGCAAGAGTT 1144

Qy 144 TTTCATGGTACACAGAGTCTCGCTGGTTGCAGCGATGCAAGAGTT 194

Db 1145 ATGGCTGGGATCTGCCAACAGGAGTCTGGCGGCGAGGGAAGCC 193

Db 1145 ATGGCTGGGATCTGGCAGGGCTGGCGGCGAGGGAAGCC 1194

Search completed: August 27, 2005, 11:33:35
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GenCore version 5.1.6
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                  Copyright
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- nucleic search, using sw model OM nucleic

August 27, 2005, 07:00:48; Search time 311.984 Seconds (without alignments) 4952.347 Million cell updates/sec о ::

Run

US-10-079-954-2

1 agccagcgaacggacgaggg.....tttacctcaagtgttgtaaa 261 Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_16Dec04:\* geneseqn1980s:\* geneseqn1990s:\* Database

geneseqn2003cs:\* geneseqn2001bs:\*geneseqn2002as:\* geneseqn2002bs:\* geneseqn2003bs:\* geneseqn2003as:\* geneseqn2001as: geneseqn2000s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003ds:\* geneseqn2004as:\*

genesegn2004bs:

# SUMMARIES

		df				
Result No.	Score	Query	Query Match Length DB	DB	ID	Description
1	256.2	98.2	261	2	AAV15589	Aav15589 Human HPK
	247.8	94	672	α	ACC51042	
ı	247.8	94.9	672	œ	ABX76400	
4	247.8	94.9	672	11	ADN39021	н
n S	247.8	94.9	754	13	ADR26553	
9	247.8	94.9	775	10	ADF60035	Adf60035 Human con
7	247.8	94.9	775	13	ADS11654	Ads11654 Human the
80	247.8	94.9	1026	7	AAV64572	Aav64572 Human Fan
σ	247.8	94.9	1373	9	ABK92263	Abk92263 Prostate
10	247.8	94.9	1373	60	ABX76167	Abx76167 Lung canc
11	247.8	94.9	1373	11	ADN39435	Adn39435 Cancer/an
12	247.8	94.9	1705	13	ADQ87331	Adq87331 Human tum
13	246.2	94.3	502	9	ABQ55843	Abq55843 Human ova
14	233.6	89.5	1745	12	ADQ24412	Adq24412 Human sof
15	175.8	67.4	748	13	ADS10353	Adel0353 Human the
16	137.8	52.8	516	10	ADF58395	Adf58395 Human pol
17	35.6	13.6	1065	4	AAS40959	Aas40959 cDNA enco
18	34.8	13.3	439	4	AAS41516	Aas41516 cDNA enco
19	34.8	13.3	1108	~	AAZ31913	Aaz31913 Human hel
20	34.8	13.3	1183	7	AAZ31920	Aaz31920 Human hel

Aak94445 Human ful Adi31205 Full leng Aaf87638 Human Rec Adr83444 Human Rec Adr83444 Human Rec Adr83494 Human Rec Aac1910 Human Nel Aaf87637 Human Rec Ac640275 Human Rec Ac640275 Human Liv Ac72844 Human Liv Ac72844 Human Liv Adc71344 Human liv Adc71344 Human liv Adc71344 Human liv Adc71344 Human liv Adc712845 Human liv Adc71284 Human liv	Adhio681 Mouse Series Continuation (6 of Continuation (16 o Continuation (6 of
4 AAK94445 12 ADI31205 AAR89638 4 AAR89638 4 AAR897636 13 AAR89344 4 AAR89637 12 ADR89394 13 ACM40275 14 AAR89633 15 ADR89535 10 ACC72844 11 ADS71346 10 ACC72843 11 ADS71346 11 ADS71346 12 ADR89552 13 AAS61210 14 AAF24856 15 ADR89552 16 AAF31938 17 ABLZ5052 18 AAR971938	12 ADH10681 12 ADN46845 05 12 ADN47591 15 12 ADN46123 05
1174 40 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2813 110000 110000
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# ALIGNMENTS

ВР AAV15589 standard; DNA; 261 RESULT 1 AAV15589

AAV15589;

(first entry) 02-JUL-1998 

Human HPK-1A C21.7 DNA.

Cervical cancer; treatment; diagnosis; passage cell; lesion; human foreskin keratinocyte cell line; HPK-1A; antibody; smear; ss.

Homo sapiens.

DE19649207-C1.

26-FEB-1998.

96DE-01049207. 96DE-01049207 27-NOV-1996; 27-NOV-1996; (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

Duerst M, Nees M;

WPI; 1998-121623/12.

Nucleic acid characteristic of late or early passage cells immortalised by papilloma virus - and related polypeptide(s) and antibodies, used for diagnosis and treatment of cervical cancer and assessing potential for progression of cervical lesions.

Claim 3; Fig 2; 8pp; German.

This sequence, C21.7, is derived from a human papillomavirus (HPV) immortalised human foreskin keratinocyte cell line HPK-1A and is characteristic of late or early passage cells. This sequence is used in a method for assessing the potential for progression of cervical lesions. Antibodies generated against the encoded polypeptide are used for diagnosis of cervical cancer and to assess potential for lesion progression. Antibodies can also be used therapeutically by inhibiting

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the polypeptide. Antisense molecules based on the nucleotide sequence are used to inhibit expression of the protein. Detecting polypeptides, or related RNA, characteristic of late passage cells (which are potentially malignant) in cervical smears is a reliable way of assessing progression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with bladder cancer-associated polynucleotide or antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention describes a method for detecting a bladder cancer-
                                                                                                                                                                    ACTTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGGG
                                                                                                                                                                                                                                   GCGATGGAGAGACCCAAGCCAGAGGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTC
                                                                                                                                                         ACTITCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCG
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                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                        Human; bladder cancer; cytostatic; gene therapy; vaccine; gene;
                                                                                                ;
                                                                            DB 2; Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                     Human bladder cancer associated cDNA sequence SEQ ID NO:172.
                                                                                               3; Indels
                                                         Sequence 261 BP; 69 A; 56 C; 77 G; 59 T; 0 U; 0 Other;
                                                                           Score 256.2; DB 2
Pred. No. 8.6e-77;
0; Mismatches 3
                                                                                                                                                                                                                                                                           TITIACCICAAGIGITGIAAA 261
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03-AUG-2001, 2001US-0310099P.
08-NOV-2001, 2001US-0343705P.
13-NOV-2001, 2001US-0350666P.
12-APR-2002, 2002US-0372246P.
                                                                                                                                                                                                                                                                                                                                             ACC51042 standard; cDNA; 672
                                                                            98.2%;
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                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                               Matches 258; Conservative
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P-PSDB; ABR48226.
                                                                             Query Match
Best Local Similarity
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                                      potential
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contacting a biological sample from the patient. The method comprises contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is 80 % identical to a ctable of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 concode the human bladder cancer-associated proteins given in ARR48146 to ABR48242). Bladder cancer-associated proteins given in ARR48146 to ABR48242). Bladder cancer-associated sequences from the present invention converted cathorities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid modecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications
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97.3%; Pred. No. 9.5e
iive 0; Mismatches
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2001US-0290492P.
2001US-0339245P.
2001US-0350666F.
2001US-0334370P.
2002US-0372246P.
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Matches 252; Conservative
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09-NOV-2001; 2
13-NOV-2001; 2
29-NOV-2001; 2
12-APR-2002; 2
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transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer, by administering a modulatory compound identified. The methods are useful cancer in a patient and for treating a mammal having lung cancer, by administering a modulatory compound identified. The methods are useful lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, dhronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and compounds that modulate lung cancer, such as antibodies. Sequences
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                                                                                                                                                                                  invention relates to a method for detecting a lung cancer-associated
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fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
                                                                                      Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITICGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:339.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 8; Length 672;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 672 BP; 136 A; 183 C; 227 G; 126 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 247.8; DB 8;
Pred. No. 9.5e-74;
0; Mismatches 7;
                                                                                                                                                        Claim 22; Page 392; 453pp; English.
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(EOSB-) EOS BIOTECHNOLOGY INC.
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                                                   WPI; 2003-093161/08
                           Murray R;
                                                               P-PSDB; ABU56671.
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention, antibodies which specifically bind a polypeptide of the invention, use of such antibodies for drug targeting, and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids polypeptides, cancer and other conditions such as psoriasis, ischeemia, heart disease, attherosclerosis, inflammatory diseases, autoimmune diseases, retinal necowascularistation syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
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                      detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CCAGCGAACGGACGAGGGTGACAATAGAGTGTGTGTCATGCTTGTGAGAGAAAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hevezi PA;
A;
retinal neovascularistaion syndrome; scarring; uterine fibroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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94.9%; Score 247.8; DB 11; Length 672;
Best Local Similarity 97.3%; Pred. No. 9.5e-74;
Matches 252; Conservative 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 672 BP; 136 A; 183 C; 227 G; 126 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gish KC, Glynne R,
Wilson KE, Zlotnik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID NO 339; 1385pp; English.
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R, Watson SR,
                                                                                                                                                                                                                                                                                                                                                                                                                               2001US-0332464P.
2001US-0334393P.
2001US-0335394P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EOSB-) EOS BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                       2002WO-US036810
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2002US-0347211P.
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2002US-0368809P.
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Mack DH, Murray R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-468649/44.
P-PSDB; ADN39022.
                                                                                                                                                                                                               WO2003042661-A2.
                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                       13-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JAN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAR-2002;
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                                                                                                 182
                                                                                                                                446
                                                                                                                                                                 242
                                                                                                                                                                                                506
                                122
                                                               386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of
TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATATAGCGGC
                                                                                                                    CGTGAAAATATTTCCACGTTTTTTCATGGTTGCGAAGCAGTGCTCCGCTGGTTGTGCAGC
                                TITCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
                                                                                                 CGTGAAAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC
                                                                                                                                                                                    GATGGAGAGACCCAAGCCCAGAGGAGAAGAGGGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT
                                                                                                                                                                 GATGGAGAGACCCAAGCCAGAGAGAGAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 247.8; DB 13; Length 754;
Pred. No. 1e-73;
0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 754 BP; 150 A; 245 C; 206 G; 153 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds; breast cancer; prognosis; gene expression; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 statistical methods of the invention. This marker used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 2414; 226pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Breast cancer prognosis marker #2414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ROSE-) RESETTA INPHARMATICS LLC. (NECA-) NETHERLANDS CANCER INST.
                                                                                                                                                                                                                               TTACCTCAAGTGTTGTAAA 261
                                                                                                                                                                                                                                                               rraccrcaagrerreraa 525
                                                                                                                                                                                                                                                                                                                                                ADR26553 standard; DNA; 754 BP
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Best Local Similarity 97.3%;
Matches 252; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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The present invention describes isolated polynuclectide sequences (I), which encode polypeptides (II) with biological activity. Also described:

(II) a vector comprising (I); (2) an expression vector comprising (I); (3)

a host cell genetically engineered to comprise (I) which is operatively
cassociated with a regulatory sequence that modulates expression of (I) in
the host cell; (4) a polypeptide (II) encoded by (I); (5) a composition
comprising the polypeptide of (4) and a carrier; (6) an antibody directed
against the polypeptide of (4); (7) detecting (I) or the polypeptide of
(4) in a sample; (8) identifying a compound that binds to the polypeptide of
(I) in producing the polypeptide of (4); (7) detecting (I) or the polypeptide of
(I) The polynucleotides (I) can be used as hybridisation probes;
(I) The polynucleotides (I) can be used as hybridisation probes;
(I) The polynucleotides (I) can be used as hybridisation probes;
(I) The polynucleotides (I) can be used as hybridisation probes;
(I) The polynucleotides (I) can be used as hybridisation probes;
(I) The polynucleotides (I) can be used as hybridisation probes;
(I) The polynucleotides (I) can be used as hybridisation probes;
(I) The polynucleotides (I) can be used as hybridisation probes;
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(I) The polynucleotides (I) can be used as hybridisation probes;
(I) The polynucleotides (I) can be used as hybridisation probes;
(I) The polynucleotides (I) can be used as hybridisation probes;
(I) The polynucleotides (I) can be used as hybridisation probes;
(I) The polynucleotides (I) can be used as hybridisation probes;
(I) The polynucleotides (I) can be used as hybridisation probes;
(I) The polynucleotides (I) can be used as hybridisation probes;
(I) The polynucleotides (II) can be used as hybridisation probes;
(I) The polynucleotides (II) can be used as hybridisation probes;
(I) The polynucleotides (II) can be used as hybridisation probes;
(I) The polynucleotides (II) can be used as hybridisation probes
                                                                                                                                                                                                              242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biological activity, genetic engineering; hybridisation probe; oligomer; primer; chromosome mapping; gene mapping; recombinant protein production;
                              TITCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGGGGC 379
                                                                                                                                                                                                                                                                259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides, useful as hybridization probes, oligomers or primers, for chromosome or gene mapping, for the recombinant production of proteins, and for generating antisense DNA or RNA.
                                                                                                                                    GATGGAGAGACCCAAGCCAGAGGAGAAGCGGTTTCTCCCTGGAAGAGCCCATGCCCTTCTT
TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
                                                                                                        123 CGTGAAAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC
                                                                                                                                                                                                              GATGGAGAGCCCAAGCCAGAGGGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human contig polynucleotide sequence SEQ ID NO:2402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ma Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weng
                                                                                                                                                                                                                                                                                                                    261
                                                                                                                                                                                                                                                                                                                                                     258 TTACCICAAGIGITGIAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2002; 2002WO-US025485.
                                                                                                                                                                                                                                                                                                                       TTACCTCAAGTGTTGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADF60035 standard; cDNA; 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001; 2001US-0311261P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; ADF60487.
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ID ADF6
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YT, D,

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DNA of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.
                                                                                                                                                                                           447 GATGGAGAGCCCAAGCCAGAGGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCTTCTT
                                                                                                                                                                     TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
                                                                                                                                                                                                                                                                                   TITICGAGIGCCAGAACCCAAGGAGGIGCAAAIGGACAGAGCCAIACIGCGITAIAGCGGC
                                                                                                                                                                                                                                                                                                                                                           387 CGTGAAAATATTTCCACGTTTTTTCATGGTTGCGAAGCAGTGCTCCGCTGGTTGTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                GATGGAGAGACCCAAGCCAGAGGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fanconi anaemia gene II; immunogen; diagnosis; detection; disease; cell cycle; disorder; cell activation; DNA repair; cytopaenia; gene therapy; tumorigenesis; ds.
                                                                                         Length 775;
                                                      Sequence 775 BP; 164 A; 209 C; 250 G; 152 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                        TITICALGETICGCAACAGGIGCICCGC
                                                                                                                              7; Indels
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                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                           Query Match 94.9%; Score 247.8; DB Best Local Similarity 97.3%; Pred. No. 1e-73; Matches 252; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Fanconi anaemia-associated gene II DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Fanconi anaemia
/note= "long reading frame'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Fanconi ana
/note= "short reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
256. .927
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P-PSDB; AAW81754.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antiinflammatory, neuroprotective, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic contig
                                                                                                                                                327 TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC 386
                                                                                                                                                                                                                                                               CGTGAAAATATTTCCACGTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC 182
                                                                                                                                                                                                                                                                                                cergaaaararrrccacerrrrrrcargerreceaaceaecrecrecresrrerecaec 446
                                                                                                                                                                                                                                                                                                                                         GATGGAGAGACCCAAGCCAGAGGAAAGCGGTTTCTCTCTGGAAGAGCCCATGCCCTTCTT 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ma Y;
3 G, Zhou
                                                                                                                                                                                     TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
                                                                                                             CCAGCGAACGGACGAGGTGACAATAGAGTGTGGGTGTCATGCTTGTGAGAGAAAACAC
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                                   Score 247.8; DB 10; Length 775; Pred. No. 1e-73;
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Weng
Sequence 775 BP; 164 A; 209 C; 250 G; 152 T; 0 U; 0 Other;
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Wang J, Ghosh M, Xue
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                                                                        0; Mismatches
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                                 Query Match 94.9%;
Best Local Similarity 97.3%;
Matches 252; Conservative
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Chen R, Zhao QA,
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P-PSDB; ADS12252
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Gish KC, Mack DH, Wilson KE,
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                                                                                                                                                                          62
                                    This sequence encodes a protein which is associated with Fanconi anaemia This protein can be used as an immunogen for preparation of antibodies. This sequence can be used for diagnosis of, or detecting predisposition to, diseases that involve disorders of the cell cycle, cell activation, cell cycle progression, DNA repair, cytopaenia, tumorigenesis and/or tumour progression, also for treatment and prevention of these diseases, particularly by gene therapy
                                                                                                                                                                                             GATGGAGAGACCCAAGCCAGAGGAGAAGAGGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT
                                                                                                                                                                                                                TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
                                                                                                                                                                                                                                  TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
                                                                                                                                                                                                                                                      CGTGAAAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC
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cycling or activation, DNA repair, cytopaenia, tumorigenesis etc
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                                                                                                                Sequence 1026 BP; 201 A; 301 C; 331 G; 191 T; 0 U; 2 Other;
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                                                                                                                                  Score 247.8; DB 2;
Pred. No. 1.1e-73;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prostate cancer-associated DNA sequence #149
                  Claim 1; Page 18-19; 35pp; German
                                                                                                                                                                                                                                                                                                                                TTACCTCAAGTGTTGTAAA 261
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08-DEC-2000; 2000US-0073342.

24-JAN-2001; 2001US-0263957P.

16-MAR-2001; 2001US-0276791P.

16-MAR-2001; 2001US-0276888P.

24-APR-2001; 2001US-0281922P.

24-APR-2001; 2001US-088474P.

30-APR-2001; 2001US-08847046.
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                                                                                                                                  Query Match

8est Local Similarity 97.3%;
Matches 252; Conservative
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gene therapy; gene;
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The present invention relates to methods of detecting a prostate cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancerassociated polymuclectides (designated PC genes) that selectively hyridise to a sequence that is at least 80% identical to them. The prostate cancerassociated polymuclectide sequences are differentially prostate cancerassociated polymuclectide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are useful for (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer associated genes are useful for diagnosing or treating prostate cancer.

as well as for identifying modulators of prostate cancer or agents that this prostate cancer. Or inhibit prostate cancer or agents that the third the prostate cancer or agents that the best of the cancer or agents that the third in gene therapy, as a vaccine or in antisense applications.

ABK92115-ABK92263 represent prostate cancer-associated polymucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lung cancer-associated polynucleotide; gene; ds; cytostatic; emphysema; antiinfilammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesson; precancerous lesson; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
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                                                                                                            Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 CCAGCGAACGACGAGGGTGACAATAGAGTGTGTGATGTTTTGTGAGAGAAAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTCGAGTGCCAGAACCCAAGGAGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 247.8; DB 6;
Pred. No. 1.3e-73;
0; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                       Claim 22; Page 426; 436pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 TIACCICAAGIGITGIAAA 261
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WPI; 2002-471335/50
                                         P-PSDB; ABG61944
                                                                                                                                                                                                                                                 prostate tissue.
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Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
                                                                                                                                                                                                                             Claim 22; Page 219-220; 453pp; English.
                                                                                                                      (EOSB-) EOS BIOTECHNOLOGY INC
                                                                  10-MAY-2001; 2001US-0290492P.
09-WOV-2001; 2001US-0339245P.
13-NOV-2001; 2001US-035666E9-
29-WOV-2001; 2001US-034370P.
12-APR-2002; 2002US-0372246P.
                                          18-APR-2002; 2002WO-US012476
                                                           2001US-0284770P
                                                                                                                                                       WPI; 2003-093161/08
                                                                                                                                        Aziz N, Murray R;
                                                                                                                                                                 P-PSDB; ABUS6446.
        WO200286443-A2
                                                          18-APR-2001;
                         31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                         invention
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polymucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell fung acancer tor other benign or precancerous lesions, e.g. atclectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polymucleotides and polypeptides are useful compounds that modulate lung cancer, such as antibodies. Sequences the invention of the invention of the compounds that modulate lung cancer, such as antibodies. Sequences the invention of the invention of the cancer of the cancer such as antibodies.

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63 TITCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC 122
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                                                                                                                                                                                                    CGTGAAAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC 182
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                                                                                                                                                              TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATATAGCGGC
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                                                                                                                                                                                                                                                                            GATGGAGAGCCAAAGCCAGAGGAGAAGCGGTTTCTCCTGGAAGAGCCCCATGCCTTCTT
                                                          Gaps
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                          94.9%; Score 247.8; DB 8; Length 1373; 97.3%; Pred. No. 1.3e-73; ive 0; Mismatches 7; Indels 0;
Sequence 1373 BP; 346 A; 324 C; 376 G; 327 T; 0 U; 0 Other;
                                        Best Local Similarity 97.3
Matches 252; Conservative
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fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis, drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine; gene; ss.
                                                               Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:A35.
                                                                                   differential expression; cancer; angiogenic disorder;
       ADN39435 standard; cDNA; 1373 BP.
                                                                                                                                                                                                                                         13-NOV-2001; 2001US-0350666P.
21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-0334393P.
03-DEC-2001; 2001US-033493P.
                                                                                                                                                                                                                                                                                                                                                                                                                               (EOSB-) EOS BIOTECHNOLOGY INC
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2002US-0347349P.
2002US-0355250P.
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2002US-0386614P.
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                                            (first entry)
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                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                         08-JAN-2002;
10-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                             12-APR-2002;
05-JUN-2002;
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29-MAR-2002;
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                                            17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                   04-APR-2002;
                                                                                                                                                                                                     22-MAY-2003.
                          ADN39435;
ADN39435
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Hevezi PA; A; Gish KC, Glynne R, Wilson KE, Zlotnik Afar D, Aziz N, Ginsburg WM, Mack DH, Murray R, Watson SR,

2003-468649/44.

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Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample. P-PSDB; ADN39436

Claim 8; SEQ ID NO A35; 1385pp; English.

whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, and the invention is the polypeptides and methods are useful for diagnosing, prognosing and treating The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprisaing: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80\%
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  ischaemia, heart disease,
                                                                                                                                                                              TTTCGAGTGCCAGAAACCCAAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
                                                                                                                                                                                                                                                                                                                                           GATGGAGAGACCCAAGCCAGAGGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT
                                                                                                                                                                                                                     TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
                                                                                                                                                                                                                                                                          CGTGAAAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC
                                                                                                                                                                                                                                                                                        GATGGAGAGACCCAAGCCCAGAGGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT
           atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistaton syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human tumour-associated antigenic target (TAT) cDNA sequence #4208.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.
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0
                                                                                                           DB 11; Length 1373;
                                                       sequence represents a nucleic acid sequence of the invention.
                                                                             Sequence 1373 BP; 346 A; 324 C; 376 G; 327 T; 0 U; 0 Other;
                                                                                                        Score 247.8; DB 11; Length
Pred. No. 1.3e-73;
0; Mismatches 7; Indels
other conditions such as psoriasis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 4208; 5504pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  TTACCTCAAGTGTTGTAAA 261
                                                                                                                                                                                                                                                                                                                                                                                                 ADQ87331 standard; cDNA; 1705 BP
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                                                                                                           94.98;
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                                                                                                                                      Matches 252; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-534300/51
                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                           Query Match
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cc sequence identity to (a) -(c); or (e) a sequence that hybridises to (a)-

(c). Also described: (1) an expression vector comprising the above

cc muclaic acid; (2) a host cell comprising the above expression vector; (3)

a process for producing a polypeptide; (4) an isolated polypeptide

cc morrising: (a) an amino acid sequence encoded by the full-

cc nuclectide sequences; (b) an amino acid sequence encoded by the full-

cc nuclectide sequences; (b) an amino acid sequence encoded by the full-

cc nuclectide sequences; (c) an entire polypeptide

cc nuclectide sequences; (b) an inno acid sequence encoded by the full-

cc nuclectide sequences; (c) a sequence

cc na isolated antibody that binds to the above polypeptide; (6)

cc no producing the antibody; (8) an isolated oligopeptide that binds to

the above polypeptide; (9) a tumour-associated antigenic target (TAT)

cc the above polypeptide; (9) a tumour-associated antigenic target (TAT)

cc the above polypeptide; (9) a tumour-associated antigenic target (TAT)

cc the above polypeptide or TAT binding organic molecule, in combination

cc antibody, oligopeptide or TAT binding organic molecule, in combination

cc mithody, oligopeptide or TAT binding organic molecule, in combination

cc mithody, oligopeptide or TAT binding organic molecule, in combination

cc mithody, oligopeptide or TAT binding organic molecule, in combination

cc mithody, oligopeptide or protein; (13) a method of a tumour in a potentiating effect of the above protein; (13) a method of determining the protein

cc therepoutically treating a mammal having a cancerous tumour comprising

cc therepoutically treating a mammal having a cancerous tumour comprising

cc therepoutically treating a mammal having a cancerous tumour comprising

cc therefore a protein in a sample suppected of containing the protein

cc mammal; (16) a method of or treating or preventing a cell proliferative

cc protein; and (17) a method of binding an antibody, oligopeptide or cc organic molecule to a cell that expresses the prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preventing or treating cancer. The composition is also used for preparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  medicament for the therapeutic treatment or diagnostic detection of a sell proliferative disorder or cancer. The present sequence represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATGGAGAGACCAAGCCAGAGGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               567 TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      627 cereaaaararrrccacerrrrrrcareerreceaaecaerecreerresrereec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 94.9%; Score 247.8; DB 13; Length 1705; Local Similarity 97.3%; Pred. No. 1.4e-73; nes 252; Conservative 0; Mismatches 7; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human TAT cDNA sequence from the present invention.
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ovarian cancer, breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysemorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gestrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss.
                                                                                                                                                                     07-JUN-2000; 2000US-0209467P.
                                                                                                                                                  07-JUN-2001; 2001WO-US018569
                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                         Birse CE, Rosen CA;
                                                                                                                                                                                                                            WPI; 2002-147878/19.
                                                                                                                                                                                                                                      P-PSDB; ABP42766.
                                                                                                              WO200200677-A1.
                                                                                             Homo sapiens.
                                                                                                                                 03-JAN-2002
                                                                                                                                                                                                                                                                                    diseases.
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Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological

Claim 1; SEQ ID NO 1723; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to CDNAs encoding them (ABQ54131-ABQ56305), and also concompasses polypeptides 90% identical and polypuclectides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen and the use of ovarian antigens polymuclectides and polympeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast related disorders. Succonditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system of sorders of ovarian or breast origin, reproductive system disorders (e.g., infertinity, disorders of pregnancy, anovulation.

CC disorders, infertinity, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infertines (e.g., chlamydia, HIV, toxoplasmosis, and toxic disorders, infertines (e.g., chlamydia, HIV, toxoplasmosis, ond toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginatory disorders (e.g., congenital and acquired immunodisorders (e.g., cancillantia, polypeptides and toxic muchanne opporatine, systemic lasorders.)

Cc shock syndromes, neurological disorders, gastrointestinal disorders condulate ovarian antigen expression or activity. The polymucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may also be used in screening for compounds which contentions and the polypeptides may be used as food additives or to prepare antibodies contential in disease disagnosis, drug targeting and phenotyping. The present contention when the represented or the printed specification, in the management of the printed specification, in the management of the printed specification, in the management of the printed specifica WIPO at ftp.wipo.int/pub/published\_pct\_sequences

Sequence 502 BP; 112 A; 125 C; 152 G; 113 T; 0 U; 0 Other;

Query Match 94.3%; Score 246.2; DB 6; Best Local Similarity 96.9%; Pred. No. 2.9e-73; Matches 251; Conservative 0; Mismatches 8;

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Indels

DB 6; Length 502;

; The invention relates to a novel method for detecting soft tissue saxcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of a gene in both samples and comparing the expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated by of the invention. The current sequence is not shown within the 182 242 TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC 122 204 264 GATGGAGACCCAAGCCAGAGGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT 324 soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human; Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue 145 TITCGAGTGCCAGAACCCAAGAGGGGGAAATGGACAGAGCCGTACTGCGTTATATAGCGGC CGTGAAAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC GATGGAGAGACCCAAGCCAGAGAGAGAGGGTTTCTCCTGGAAGAGCCCCATGCTT 1; Gaps DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor. 89.5%; Score 233.6; DB 12; Length 1745; 96.2%; Pred. No. 9.9e-69; ive 0; Mismatches 9; Indels 1; Sequence 1745 BP; 402 A; 455 C; 511 G; 377 T; 0 U; 0 Other; Human soft tissue sarcoma-upregulated DNA - SEQ ID 7232. Example 2; SEQ ID NO 7232; 210pp; English. Zlotník A; 261 325 rraccrcaagrerreraa 343 BP. (PROT-) PROTEIN DESIGN LABS INC. TTACCTCAAGTGTTGTAAA 26-NOV-2003; 2003WO-US038193. 26-NOV-2002; 2002US-0429739P. ADQ24412 standard; DNA; 1745 (first entry) Query Match 89.5 Best Local Similarity 96.2 Matches 250; Conservative Aziz N, Ginsburg WM, WPI; 2004-441208/41. WO2004048938-A2. Homo sapiens. 26-AUG-2004 10-JUN-2004. 205 ADQ24412; 63 123 183 265 243 RESULT 14 ADQ2441; 유 ò 셤 δ 셤 ò 셤 

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989
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Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
62
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                                                                                                                                                                                                                                       CCGTGAAAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAG
                                                                                                                                                                                                                                                                                                                     CGATGGAGACCCAAAGCCAGAGAGAAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTCT
                                                                                                                                                                                                                                                                                                                                                   CGATGGAGAGAGCCAGAGGGGGAGAAGGGGTTTCTCCTGGAAGAGGCCCATGCTTCT
                                                                                                       -TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human therapeutic DNA - SEQ ID 590
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Chen R, Zhao QA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antinflammatory, neuroprotective, antianaemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, hacmatopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic DNA of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.

Claim 1; SEQ ID NO 590; 718pp; English

Sequence 748 BP; 157 A; 207 C; 246 G; 138 T; 0 U; 0 Other;

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1;
                                                                                                                                                      122
                                                                                      338 TITICGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGGCCATACTGCGTTATAGGGGC 397
                                                                                                                 CGTGAAAATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGC 182
                                                                                                                             TTTCGAGTGCCAGAACCCAAGGAGGTGCAAATGGACAGAGCCATACTGCGTTATAGCGGC
                                      Gaps
                    35;
  Length 748;
Score 175.8; DB 13; Length
Pred. No. 3.5e-49;
0; Mismatches 2; Indels
                                                                                                                                                                                                261
                                                                                                                                                                                                243 TTACCTCAAGTGTTGTAAA
 Query Match
Best Local Similarity 85.7%;
Matches 222; Conservative
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completed: August 27, 2005, 08:59:49 Search com Job time :

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

August 27, 2005, 08:48:34 Run on:

' Search time 93.5484 Seconds
(without alignments)
4565.212 Million cell updates/sec

US-10-079-954-2

261 score: Title: Perfect

1 agccagcgaacggacgaggg.....tttacctcaagtgttgtaaa 261 Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1202784 seqs, 818138359 residues Searched:

2405568 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*
/cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*
/cgn2\_6/prodata/1/ina/6A\_COMB.seq:\*
/cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*
/cgn2\_6/prodata/1/ina/PcTUS\_COMB.seq:\*
/cgn2\_6/prodata/1/ina/PcTUS\_COMB.seq:\* Issued Patents NA:\* ......... Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		df			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	Description
1	261	100.0	261	m	US-09-308-984-2	Sequence 2, Appli
7	35.6	13.6	399	4	US-09-621-976-8976	897
က	34.8	13.3	1233	4	US-09-949-016-3456	3456
4	ω.	13.0	1260	4	US-09-949-016-1949	
ហ	33.8	13.0	1337	4	US-09-127-928-1	
9	33.8	13.0	8572	4	US-09-949-016-13691	Sequence 13691, A
7	31.2	12.0	114793	4	US-10-148-806-3	
8	30.6	11.7	251769	4	US-09-949-016-13185	131
0 0	30.6	,11.7	251769	4	US-09-949-016-13186	1318
c 10	30.6	11.7	266748	4	19-949-016-	Sequence 13187, A
c 11	30.6	11.7	266748	4	US-09-949-016-13188	_
12	30.4	11.6	5157	~	US-08-474-169-7	Sequence 7, Appli
13	30.4	11.6	œ	4	US-09-949-016-15881	15
14	30.2	11.6		4	US-09-949-016-16066	16066,
	30.2	11.6	784019	4	US-09-949-016-14033	Sequence 14033, A
c 16	30.2	11.6	828152	4	US-09-949-016-12777	
17	30	11.5	601	4	US-09-949-016-141144	Sequence 141144,
18	30	11.5	1541	4	US-09-270-767-11220	Sequence 11220, A
19	30	11.5	9386	4	US-09-949-016-15739	Sequence 15739, A
20	29.8	11.4	632	н	US-08-580-038-65	Sequence 65, Appl
21	29.6	11.3	735	4	-60	Sequence 1496, Ap
c 22	29.6	11.3	1550	4	US-09-976-594-766	766,
23	29.4	11.3	1512	4	US-09-107-532A-54	54,
c 24	6	11.3	49225	4	US-09-902-540-1269	126
52	29	11.1	289	ო	US-09-007-005-17	17,
56	29	11.1	289	т	US-09-244-796-17	17,
27	29	11.1	1313	4	US-09-023-655-59	Sequence 59, Appl

Sequence 820, App Sequence 10615, A	Sequence 1063, Ap	Sequence 13, Appl	Sequence 9, Appli	Sequence 11, Appl	Sequence 7, Appli	Sequence 1, Appli	Sequence 13053, A	Sequence 1, Appli	Sequence 203508,	Sequence 15, Appl	Sequence 15, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 17486, A
US-09-221-017B-820 US-09-621-976-10615	US-09-620-312D-1063	US-10-265-012-13	US-10-265-012-9	US-10-265-012-11	US-10-265-012-7	US-10-265-012-1	US-09-949-016-13053	3 US-09-103-84:0A-1	US-09-949-016-203508	US-08-901-200A-15	US-09-219-391-15	. US-08-480-528A-11	. US-08-479-666-11	. PCT-US93-10520-11	US-09-949-016-17486
5860 3 480 4	3001 4	1116 4	1302 4	1521 4	1707 4	1824 4	30337 4	4411529	601 4	4584 2	4584 3	6418 1	6418 1	6418 5	56976 4
11.1	11.0	10.9	10.9	10.9	10.9	10.9	10.9		10.8	10.8	10.8	10.8	10.8	10.8	10.8
28.8	28.8	28.4	28.4	28.4	28.4	28.4	28.4	28.4	28.2	28.2	28.2	28.2	28.2	28.2	28.2
c 28	0 0 31	32	c 33	c 34	c 35	c 36	c 37	c 38	c 39	40	41	42	. 43	44	c 45

# ALIGNMENTS

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Sequence 2, Application US/09308984

Patent No. 6388065

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nees, Matthias
APPLICANT: Nees, Matthias
APPLICANT: Nees, Matthias
APPLICANT: Nees, Matthias
TITLE OF INVENTION: DNA FOR EVALUATING THE PROGRESSION POTENTIAL OF CERVICAL LESIONS
TILE REPERENCE: SCHU 204 (09902857)
CURRENT APPLICATION NUMBER: US/09/3308,984
CURRENT FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: DE 196-11-12
PRIOR APPLICATION NUMBER: DE 196-11-12
PRIOR APPLICATION NUMBER: DE 196-11-12
PRIOR FILING DATE: 1997-11-27
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 2
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100.0%; Score 261; DB 3;
Best Local Similarity 100.0%; Pred. No. 3.5e-82;
Matches 261; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 rirraccicaagrerigiaaa 261
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                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-308-984-2
US-09-308-984-2
                                                                                                                                                                                                                                                                                                                                                LENGTH: 261
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RESULT 2 US-09-621-976-8976 ; Sequence 8976, Application US/09621976

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1018 ATGGCTGCGTACTACCAGGAGTCTGGCCGGCTGGCAGGGATGGGAAGCC 1067
                                                                                                           Sequence 1949, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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1 Similarity 53.4%;
71; Conservative
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; LOCATION: (170)..(1066)
US-09-127-928-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) ORGANISM: Human
US-09-949-016-1949
                                                                                             US-09-949-016-1949
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US-09-127-928-1
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Best Local S
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Sequence 3456, Application US/09949016

Setent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NOS: 207012

SEQ ID NOS: 207012

SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 YAWMYYMMARRITWWGMRASCYRGAYMASAGMYYWMYYWMRRKWMYSAGWSMMRKWTRRC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 ATATTTCCACGTTTTTTCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGCGATGGAG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 WMKKRRRRRRAWMWKSMCWMKKSKSWWRSWGMMTKRMKGRGAASWAGYMSWMTYMTRRW 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 ACGACGAGGGTGACAATAGAGTGTGTGTCATGCTTGTGAGAGAAAACACTTTCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 ASYSCHSSYCHWGAKMOMYWKISRWSYWSSYRCIKYRRSCCCWSMSCYWKTYY 273
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
13.6%; Score 35.6; DB 4; Length 399;
Best Local Similarity 12.4%; Pred. No. 0.023;
Matches 29; Conservative 108; Mismatches 97; Indels
                                                                APPLICANT: Jobert, S. APPLICANT: Jobert, S. APPLICANT: Glordano, J.Y. TITLE OF INVENTION: ESTE and Encoded Human Proteins. FILE REFERENCE: GENSET.054RR2 CURRENT APPLICATION NUMBER: US/09/621,976 CURRENT FILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 19335 SOFTWARE: Patent.pm SEQ ID NOS: 19335 SOFTWARE: Patent.pm
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-8976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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ORGANISM: Human
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US-09-949-016-3456
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| Sequence 1, Application US/09127928
| Sequence 1, Application US/09127928
| Patent No. 6472172
| GENERAL INFORMATION:
| APPLICANT: Deng, Gang
| APPLICANT: Morser, Michael J
| TITLE OF INVENTION: DNA Encoding a No. 6472172el Human Inhibitor-of-Apoptosis
| TITLE OF INVENTION: DNA Encoding HIAP3
| CURRENT APPLICATION NUMBER: US/09/127,928
| CURRENT APPLICATION NUMBER: US/09/127,928
| CURRENT PILING DATE: 1998-07-31
| NUMBER OF SEQ ID NOS: 7
| SEQ TO NO 1
| SEQ TO NO 1
| LINGTH: 1337
APPLICANT: VENTILE.

APPLICANT: VENTILE.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FABLEEQ for Windows Version 4.0

SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 CGCAACAGGTGCTCCGCTGGTTGTGCAGCGATGGAGAGACCCAAGCCAAGGCGAGAAGCGG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 gaccacadeceaeccacresecaeccesrearesreceaececaesaececrereseaecec 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33.8; DB 4; Length 1260;
Pred. No. 0.17;
0; Mismatches 62; Indels 0
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 52.8
Matches 66; Conservative
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                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-148-806-3
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US-09-949-016-13185/c
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ORGANISM: Human
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                                             SEO ID NO 3
LENGTH: 114793
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Fatent No. 6812339
GENERAL INFORMATION:
FATENCE OF INVENTION:
FAPILCANT: VERPER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR RELICATION NUMBER: 60/231,498
FRIOR RELICATION NUMBER: 60/231,498
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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94 TGGACAGAGCCATACTGCGTTATAGCGGCCGTGAAAATATTTCCACGTTTTTTCATGGTT 153
                                                                                     147 redresas de concercentes de consecuencia d
                                                                                                                                                                           154 CGCAACAGGTGCTCCGCTGGTTGTGCAGCGATGGAGAGCCCAAGCCAGAGGAGAAGCGG 213
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Patent No. 6762042

Patent No. 6762042

JERBERAL INFORMATION:
APPLICANT: BIA: Chang
APPLICANT: Metzger, Michael
APPLICANT: Liu, Xiaomeil
APPLICANT: Liu, Xiaomeil
APPLICANT: Liu, Xiaomeil
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
TITLE OP INVENTION: HELICASE
PILE REFERENCE: 20585P
CURRENT FILING DATE: 2006-05
PRIOR APPLICATION NUMBER: US00/33065
PRIOR APPLICATION NUMBER: 60/169,970
PRIOR PILING DATE: 1999-12-09
NUMBER OF SEQ ID NOS: 38
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13.0%; Score 33.8; Di
Best Local Similarity 53.4%; Pred. No. 0.46
Matches 71; Conservative 0; Mismatches
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; ORGANISM: Human
US-09-949-016-13691
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RESULT 9
US-099-016-13186/c
iSequence 13186 Application US/09949016
iSequence 13186 Application US/09949016
iSequence 13186.
iSequence 13186 Application US/09949016
iSequence 13186 Application US/09949016
iSequence 13186 Application US/09/949,016
iSETILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
iSETILE REPERENCE: CL001307
iSCURRENT APPLICATION NUMBER: US/09/949,016
iSCURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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                                                                                                                                                                                               43606 CCTGGTAGGCAAACGGAGCGTCTTTGCCATTGCAGGGATGAAGCCACCGAGGCAGGAGA 43665
                                                                                                                                          147 CATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGCGATGGAGGACCCAAAGCCAGAGGA
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Score 31.2; DB 4; Length 114793; Pred. No. 14; 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 251769;
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                                                                                                                                                                                                                                                                                                                                  43666 AAAGTGCTTTGCCCTACAAGCAACTAAGTCAT 43697
                                                                                                                                                                                                                                                                             207 GAAGCGGTTTCTCCTGGAAGAGCCCATGCCCT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TILE KEFERENCE CUOLUSO
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
SPIOR FILING DATE: 2000-10-03
SOFTWARE: PAGES OF WINDER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 13185, Application US/09949016
; Patent No. 6812339
   Query Match
Best Local Similarity 58.7%;
Matches 54; Conservative (
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US-09-949-016-13188
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US-08-474-169-7
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Best Local S
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| Sequence 13187, Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE OF INVENTION: WINDER: 60/29,016 |
| CURRENT APPLICATION NUMBER: 60/241,755 |
| PRIOR APPLICATION NUMBER: 60/231,768 |
| PRIOR FILLING DATE: 2000-10-03 |
| PRIOR FILLING DATE: 2000-10-03 |
| PRIOR FILLING DATE: 2000-09-08 |
| NUMBER OF SEQ 1D NOS: 207012 |
| SEQ 1D NO 13187 |
| LENGTH: 266748 |
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Best Local Similarity 52.8%; Pred. No. 35;
Matches 66; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.7%; Score 30.6; DB
52.8%; Pred. No. 34;
tive 0; Mismatches
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 13186
LENGTH: 251769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 52.84
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218156 AAACA 218152
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US-09-949-016-13187/c
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US-09-949-016-13186
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US-09-949-016-13187
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US-09-949-016-13188/C
; Sequence 13188, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218241 GTATCTTGATTCATACAĞATATACTATTTTTCAĞAĞCAAĞAAAGAGAĞGĞACAATAAA 218182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Schatz, David G.
TITLE OF INVENTION: An Autoregulatory Tetracycline-Regulated
TITLE OF INVENTION: An Autoregulatory Tetracycline-Regulated
TITLE OF INVENTION: System for Inducible Gene Expression in Eucaryotes
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STERET: 1100 New York Ave. Suite 600
CITY: Washington
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 GTGTCATGCTTGTGAGAGAGAAAACACTTTCGAGTGCCAGAACCCAAGGAGGTGCAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 GACAGAGCCATACTGCGTTATAGCGGCCGTGAAAATATTTCCACGTTTTTTCATGGTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 266748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER TREADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COMPUTER: DEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION: 435
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30.6; DI
Pred. No. 35;
0; Mismatches
                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-175
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13188
LENGTH: 266748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 7, Application US/08474169
; Patent No. 5851796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.7%;
52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 52.8 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218121 AAACA 218117
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FEATURE
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Sequence 15881 Application US/09949016

Sequence 15881 Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENCE: CLOA01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTESEQ for Windows Version 4.0

SEQ ID NO 15881

LENGTH: 87470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17392 AAATGTTCAAGGTGATACTTAGTTTTAACTGCCTTGACAGTGTTCTTTTTTTGTTTTTTT 17451
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                                                                                                                                                                                                                                                                                                               131 TATTICCACGITITITCATGGTTCGCAACAGGTGCTCCGCTGGTTGTGCAGCGATGGAGA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 AAATGGACAGAGCCATACTGCGTTATAGCGGCCGTGAAAATATTTCCACGTTTTTTCATG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 GTTCGCAACAGGTGCTCCGCTGGTTGTGCAGCGATGGAGAGCCCAAGCCAAGGAAGAAG 210
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                   3107 GGCCAACGCGCGGAGAGGCGGTTTGCGTATTGGGCTCTTCCGCTTCCT 3158
                                                                                                                                                                                                                                                                                                                                                         191 GACCCAAGCCAGAGAGAGCGGTTTCTCCTGGAAGAGCCCATGCCCTTCTT 242
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                                                                                                                                                                                        Length 5157;
                                                                                                                                                                                                                                51; Indels
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                                                                                                                                                                                        DB 2;
                                                                                                                                                                                    Query Match
11.6%; Score 30.4; DE
Best Local Similarity 54.5%; Pred. No. 5.7;
Matches 61; Conservative. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)....(87470)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15881
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                                                                                                  CDS
502..2184
                   both
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nucleic acid
                                       TOPOLOGY: both MOLECULE TYPE: cDNA
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Matches 79; Conserva
                   STRANDEDNESS:
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US-09-949-016-15881
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                                                                                                ; NAME/KEY:
; LOCATION:
US-08-474-169-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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US-09-949-016-16066
Sequence 16066, Application US/09949016
Parent No. 6812339
GENERAL INFORMATION:

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FARENAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT FILING DATE: 2000-04-14

FRIOR APPLICATION NUMBER: 60/231,756

PRIOR APPLICATION NUMBER: 60/231,756

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 14033

LENGTH: 784019
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 00/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-30
PRIOR PLING DATE: 2000-0-0-09
RIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         326015 AGGGTGAAACAAAGGAGTGTAAAAATGCTAGAATTTACCCAATCAGTACACACAGGGTCAGT 325956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27633 TTGAAATTGGTGTTATGTTCATGGTAGAGCCAACAGGATTTACTGGTAGATAGGTAAGGG 27692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 TAGAGIGIGGIGICATGCTIGIGAGAGAAAACACTITICGAGIGCCAGAACCCAAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27693 GIGIAAGAGGAGICAAGCAIACTGIGIAAGA 27723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 GTGCAAATGGACAGAGCCATACTGCGTTATA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30.2; DB Pred. No. 36; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 11.6%; Score 30.2; I
Best Local Similarity 51.1%; Pred. No. 82;
Matches 71; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14033, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; LOCATION: (1)...(144362)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16066
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| NAME/KEY: misc_feature
| LOCATION: (1)...(784019)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.6%;
58.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 58.2
Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 144362
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